

# SEQUENCE LISTING

## (1) GENERAL INFORMATION

- 5 (i) APPLICANT: Alvarez, Vernon L.  
O'Mahony, Daniel J.  
Lambkin, Imelda J.  
Singleton, Judith  
Patterson, Catherine A.  
Cagney, Gerard M.  
Belinka, Benjamin A.  
Carter, John M.
- 10 (ii) TITLE OF THE INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-  
INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS
- (iii) NUMBER OF SEQUENCES: 265
- 15 (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pennie & Edmonds LLP  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: USA  
(F) ZIP: 10036
- 20 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- 25 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Misrock, S. Leslie  
(B) REGISTRATION NUMBER: 18,872  
(C) REFERENCE/DOCKET NUMBER: 1101-220
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 212-790-9090  
(B) TELEFAX: 212-869-9741  
(C) TELEX: 66141 PENNIE

## (2) INFORMATION FOR SEQ ID NO:1:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Gly | Ala | Tyr | Glu | Ser | Pro | Asp | Gly | Arg | Gly | Gly | Arg | Ser | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Gly | Gly | Gly | Gly | Gly | Cys | Gly | Asn | Ile | Gly | Arg | Lys | His | Asn | Leu |

20 25 30  
 Trp Gly Leu Arg Thr Ala Ser Pro Ala Cys Trp Asp  
 35 40

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10 Ser Pro Arg Ser Phe Trp Pro Val Val Ser Arg His Glu Ser Phe Gly  
 1 5 10 15  
 Ile Ser Asn Tyr Leu Gly Cys Gly Tyr Arg Thr Cys Ile Ser Gly Thr  
 20 25 30  
 Met Thr Lys Ser Ser Pro Ile Tyr Pro Arg His Ser  
 35 40

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20 Ser Ser Ser Ser Asp Trp Gly Gly Val Pro Gly Lys Val Val Arg Glu  
 1 5 10 15  
 Arg Phe Lys Gly Arg Gly Cys Gly Ile Ser Ile Thr Ser Val Leu Thr  
 20 25 30  
 Gly Lys Pro Asn Pro Cys Pro Glu Pro Lys Ala Ala  
 35 40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 Arg Val Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg  
 1 5 10 15  
 Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly  
 20 25 30  
 Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Ala His  
 35 40

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu  
1 5 10 15  
Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro  
20 25 30  
Gln Leu Pro Arg Gly Pro Asn  
35

(2) INFORMATION FOR SEQ ID NO:6:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

15 Ser Pro Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe  
1 5 10 15  
Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala  
20 25 30  
Ser Leu Glu Pro Pro Ser Ser Asp Tyr  
35 40

(2) INFORMATION FOR SEQ ID NO:7:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Gly Ala Ala Asp Gln Arg Arg Gly Trp Ser Glu Asn Leu Gly Leu  
1 5 10 15  
Pro Arg Val Gly Trp Asp Ala Ile Ala His Asn Ser Tyr Thr Phe Thr  
20 25 30  
Ser Arg Arg Pro Arg Pro Pro  
35

30 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Gly Glu Val Ser Ser Trp Gly Arg Val Asn Asp Leu Cys Ala  
1 5 10 15

Arg Val Ser Trp Thr Gly Cys Gly Thr Ala Arg Ser Ala Arg Thr Asp  
 20 25 30  
 Asn Lys Gly Ph Leu Pro Lys His Ser Ser Leu Arg  
 35 40

(2) INFORMATION FOR SEQ ID NO:9:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

10 Ser Asp Ser Asp Gly Asp His Tyr Gly Leu Arg Gly Gly Val Arg Cys  
 1 5 10 15  
 Ser Leu Arg Asp Arg Gly Cys Gly Leu Ala Leu Ser Thr Val His Ala  
 20 25 30  
 Gly Pro Pro Ser Phe Tyr Pro Lys Leu Ser Ser Pro  
 35 40

(2) INFORMATION FOR SEQ ID NO:10:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20 Arg Ser Leu Gly Asn Tyr Gly Val Thr Gly Thr Val Asp Val Thr Val  
 1 5 10 15  
 Leu Pro Met Pro Gly His Ala Asn His Leu Gly Val Ser Ser Ala Ser  
 20 25 30  
 Ser Ser Asp Pro Pro Arg Arg  
 35

(2) INFORMATION FOR SEQ ID NO:11:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30 Arg Thr Thr Thr Ala Lys Gly Cys Leu Leu Gly Ser Phe Gly Val Leu  
 1 5 10 15  
 Ser Gly Cys Ser Phe Thr Pro Thr Ser Pro Pro Pro His Leu Gly Tyr  
 20 25 30  
 Pro Pro His Ser Val Asn  
 35

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5  
 Ser Pro Lys Leu Ser Ser Val Gly Val Met Thr Lys Val Thr Glu Leu  
 1 5 10 15  
 Pro Thr Glu Gly Pro Asn Ala Ile Ser Ile Pro Ile Ser Ala Thr Leu  
 20 25 30  
 Gly Pro Arg Asn Pro Leu Arg  
 35

(2) INFORMATION FOR SEQ ID NO:13:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Trp Cys Gly Ala Glu Leu Cys Asn Ser Val Thr Lys Lys Phe Arg  
 1 5 10 15  
 Pro Gly Trp Arg Asp His Ala Asn Pro Ser Thr His His Arg Thr Pro  
 20 25 30  
 Pro Pro Ser Gln Ser Ser Pro  
 35

(2) INFORMATION FOR SEQ ID NO:14:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Trp Cys Gly Ala Asp Asp Pro Cys Gly Ala Ser Arg Trp Arg Gly  
 1 5 10 15  
 Gly Asn Ser Leu Phe Gly Cys Gly Leu Arg Cys Ser Ala Ala Gln Ser  
 20 25 30  
 Thr Pro Ser Gly Arg Ile His Ser Thr Ser Thr Ser  
 35 40

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Lys Ser Gly Glu Gly Gly Asp Ser Ser Arg Gly Glu Thr Gly Trp

1 5 10 15  
Ala Arg Val Arg Ser His Ala Met Thr Ala Gly Arg Phe Arg Trp Tyr  
20 25 30  
Asn Gln Leu Pro Ser Asp Arg  
35

(2) INFORMATION FOR SEQ ID NO:16:

5

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Ser Ser Ala Asn Asn Cys Glu Trp Lys Ser Asp Trp Met Arg Arg  
1 5 10 15  
Ala Cys Ile Ala Arg Tyr Ala Asn Ser Ser Gly Pro Ala Arg Ala Val  
20 25 30  
Asp Thr Lys Ala Ala Pro  
35

15 (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser Lys Trp Ser Trp Ser Ser Arg Trp Gly Ser Pro Gln Asp Lys Val  
1 5 10 15  
Glu Lys Thr Arg Ala Gly Cys Gly Gly Ser Pro Ser Ser Thr Asn Cys  
20 25 30  
His Pro Tyr Thr Phe Ala Pro Pro Pro Gln Ala Gly  
35 40

25

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser Gly Phe Trp Glu Phe Ser Arg Gly Leu Trp Asp Gly Glu Asn Arg  
1 5 10 15  
Lys Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser Ala Gln Gly  
20 25 30  
Pro Cys Pro Val Thr Pro Ala Thr Ile Asp Lys His  
35 40

35

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Ser Glu Ser Gly Arg Cys Arg Ser Val Ser Arg Trp Met Thr Thr Trp
 1           5           10           15
Gln Thr Gln Lys Gly Gly Cys Gly Ser Asn Val Ser Arg Gly Ser Pro
          20           25           30
Leu Asp Pro Ser His Gln Thr Gly His Ala Thr Thr
          35           40

```

10 (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Arg Glu Trp Arg Phe Ala Gly Pro Pro Leu Asp Leu Trp Ala Gly Pro
 1           5           10           15
Ser Leu Pro Ser Phe Asn Ala Ser Ser His Pro Arg Ala Leu Arg Thr
          20           25           30
Tyr Trp Ser Gln Arg Pro Arg
          35

```

20 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Arg Met Glu Asp Ile Lys Asn Ser Gly Trp Arg Asp Ser Cys Arg Trp
 1           5           10           15
Gly Asp Leu Arg Pro Gly Cys Gly Ser Arg Gln Trp Tyr Pro Ser Asn
          20           25           30
Met Arg Ser Ser Arg Asp Tyr Pro Ala Gly Gly His
          35           40

```

30 (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser His Pro Trp Tyr Arg His Trp Asn His Gly Asp Phe Ser Gly Ser  
 1 5 10 15  
 Gly Gln Ser Arg His Thr Pro Pro Glu Ser Pro His Pro Gly Arg Pro  
 20 25 30  
 Asn Ala Thr Ile  
 35

5 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser  
 1 5 10 15  
 Ser Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala  
 20 25 30  
 Gly Arg Gly Pro Arg Gly Thr Met Val Ser Arg Leu  
 35 40

15 (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Gln Gly Ser Lys Gln Cys Met Gln Tyr Arg Thr Gly Arg Leu Thr  
 1 5 10 15  
 Val Gly Ser Glu Tyr Gly Cys Gly Met Asn Pro Ala Arg His Ala Thr  
 20 25 30  
 Pro Ala Tyr Pro Ala Arg Leu Leu Pro Arg Tyr Arg  
 35 40

25 (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Gly Arg Thr Thr Ser Glu Ile Ser Gly Leu Trp Gly Trp Gly Asp  
 1 5 10 15  
 Asp Arg Ser Gly Tyr Gly Trp Gly Asn Thr Leu Arg Pro Asn Tyr Ile  
 20 25 30  
 Pro Tyr Arg Gln Ala Thr Asn Arg His Arg Tyr Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:26:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Trp Asn Trp Thr Val Leu Pro Ala Thr Gly Gly His Tyr Trp Thr  
1 5 10 15  
Arg Ser Thr Asp Tyr His Ala Ile Asn Asn His Arg Pro Ser Ile Pro  
20 25 30  
His Gln His Pro Thr Pro Ile  
35

10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Trp Ser Ser Trp Asn Trp Ser Ser Lys Thr Thr Arg Leu Gly Asp  
1 5 10 15  
Arg Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro  
20 25 30  
Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Thr  
35 40

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Gly Ser Leu Asn Ala Trp Gln Pro Arg Ser Trp Val Gly Gly Ala  
1 5 10 15  
Phe Arg Ser His Ala Asn Asn Asn Leu Asn Pro Lys Pro Thr Met Val  
20 25 30  
Thr Arg His Pro Thr  
35

30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg Tyr Ser Gly Leu Ser Pro Arg Asp Asn Gly Pro Ala Cys S r Gln  
 1 5 10 15  
 Glu Ala Thr Leu Glu Gly Cys Gly Ala Gln Arg Leu Met S r Thr Arg  
 20 25 30  
 Arg Lys Gly Arg Asn Ser Arg Pro Gly Trp Thr Leu  
 35 40

5 (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Val Gly Asn Asp Lys Thr Ser Arg Pro Val Ser Phe Tyr Gly Arg  
 1 5 10 15  
 Val Ser Asp Leu Trp Asn Ala Ser Leu Met Pro Lys Arg Thr Pro Ser  
 20 25 30  
 Ser Lys Arg His Asp Asp Gly  
 35

15 (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Arg Trp Pro Ser Val Gly Tyr Lys Gly Asn Gly Ser Asp Thr Ile Asp  
 1 5 10 15  
 Val His Ser Asn Asp Ala Ser Thr Lys Arg Ser Leu Ile Tyr Asn His  
 20 25 30  
 Arg Arg Pro Leu Phe Pro  
 35

25 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Arg Thr Phe Glu Asn Asp Gly Leu Gly Val Gly Arg Ser Ile Gln Lys  
 1 5 10 15  
 Lys Ser Asp Arg Trp Tyr Ala Ser His Asn Ile Arg Ser His Phe Ala  
 20 25 30  
 35 Ser Met Ser Pro Ala Gly Lys  
 35

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Tyr Cys Arg Val Lys Gly Gly Gly Glu Gly Gly His Thr Asp Ser  
1 5 10 15  
Asn Leu Ala Arg Ser Gly Cys Gly Lys Val Ala Arg Thr Ser Arg Leu  
20 25 30  
Gln His Ile Asn Pro Arg Ala Thr Pro Pro Ser Arg  
35 40

10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Trp Thr Arg Trp Gly Lys His Thr His Gly Gly Phe Val Asn Lys  
1 5 10 15  
Ser Pro Pro Gly Lys Asn Ala Thr Ser Pro Tyr Thr Asp Ala Gln Leu  
20 25 30  
Pro Ser Asp Gln Gly Pro Pro  
35

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Gln Val Asp Ser Phe Arg Asn Ser Phe Arg Trp Tyr Glu Pro Ser  
1 5 10 15  
Arg Ala Leu Cys His Gly Cys Gly Lys Arg Asp Thr Ser Thr Thr Arg  
20 25 30  
Ile His Asn Ser Pro Ser Asp Ser Tyr Pro Thr Arg  
35 40

30

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Phe Leu Arg Ph Gln Ser Pro Arg Phe Glu Asp Tyr S r Arg Thr  
 1 5 10 15  
 Ile Ser Arg Leu Arg Asn Ala Thr Asn Pro Ser Asn Val Ser Asp Ala  
 20 25 30  
 His Asn Asn Arg Ala Leu Ala  
 35

5 (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Ser Ile Thr Asp Gly Gly Ile Asn Glu Val Asp Leu Ser Ser Val  
 1 5 10 15  
 Ser Asn Val Leu Glu Asn Ala Asn Ser His Arg Ala Tyr Arg Lys His  
 20 25 30  
 Arg Pro Thr Leu Lys Arg Pro  
 35

15 (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Ser Lys Val Ser Ser Pro Arg Asp Pro Thr Val Pro Arg Lys Gly  
 1 5 10 15  
 Gly Asn Val Asp Tyr Gly Cys Gly His Arg Ser Ser Ala Arg Met Pro  
 20 25 30  
 Thr Ser Ala Leu Ser Ser Ile Thr Lys Cys Tyr Thr  
 35 40

25 (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Arg Ala Ser Thr Gln Gly Gly Arg Gly Val Ala Pro Glu Phe Gly Ala  
 1 5 10 15  
 Ser Val Leu Gly Arg Gly Cys Gly Ser Ala Thr Tyr Tyr Thr Asn Ser  
 20 25 30  
 35 Thr Ser Cys Lys Asp Ala Met Gly His Asn Tyr Ser  
 35 40

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Arg Trp Cys Glu Lys His Lys Phe Thr Ala Ala Arg Cys Ser Ala Gly  
 1 5 10 15  
 Ala Gly Phe Glu Arg Asp Ala Ser Arg Pro Pro Gln Pro Ala His Arg  
 20 25 30  
 Asp Asn Thr Asn Arg Asn Ala  
 35

10

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Phe Gln Val Tyr Pro Asp His Gly Leu Glu Arg His Ala Leu Asp  
 1 5 10 15  
 Gly Thr Gly Pro Leu Tyr Ala Met Pro Gly Arg Trp Ile Arg Ala Arg  
 20 25 30  
 Pro Gln Asn Arg Asp Arg Gln  
 35

20

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Arg Cys Thr Asp Asn Glu Gln Cys Pro Asp Thr Gly Thr Arg Ser  
 1 5 10 15  
 Arg Ser Val Ser Asn Ala Arg Tyr Phe Ser Ser Arg Leu Leu Lys Thr  
 20 25 30  
 His Ala Pro His Arg Pro  
 35

30

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Ala Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg  
 1 5 10 15  
 Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn  
 20 25 30  
 Pro Arg Gly Arg Arg His Pro  
 35

5 (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Ser Ala Asp Ala Glu Lys Cys Ala Gly Ser Leu Leu Trp Trp Gly  
 1 5 10 15  
 Arg Gln Asn Asn Ser Gly Cys Gly Ser Pro Thr Lys Lys His Leu Lys  
 20 25 30  
 His Arg Asn Arg Ser Gln Thr Ser Ser Ser Ser His  
 35 40

15 (2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Arg Pro Lys Asn Val Ala Asp Ala Tyr Ser Ser Gln Asp Gly Ala Ala  
 1 5 10 15  
 Ala Glu Glu Thr Ser His Ala Ser Asn Ala Ala Arg Lys Ser Pro Lys  
 20 25 30  
 His Lys Pro Leu Arg Arg Pro  
 35

25 (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Gly Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn  
 1 5 10 15  
 Leu His Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr  
 20 25 30  
 35 Pro Ser Asn Arg Gly His Lys  
 35

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Arg Trp Gly Trp Glu Arg Ser Pro Ser Asp Tyr Asp Ser Asp Met Asp  
1 5 10 15  
Leu Gly Ala Arg Arg Tyr Ala Thr Arg Thr His Arg Ala Pro Pro Arg  
20 25 30  
Val Leu Lys Ala Pro Leu Pro  
35

10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Arg Gly Trp Lys Cys Glu Gly Ser Gln Ala Ala Tyr Gly Asp Lys Asp  
1 5 10 15  
Ile Gly Arg Ser Arg Gly Cys Gly Ser Ile Thr Lys Asn Asn Thr Asn  
20 25 30  
His Ala His Pro Ser His Gly Ala Val Ala Lys Ile  
35 40

20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Arg Glu Glu Ala Asn Trp Asp Gly Tyr Lys Arg Glu Met Ser His  
1 5 10 15  
Arg Ser Arg Phe Trp Asp Ala Thr His Leu Ser Arg Pro Arg Arg Pro  
20 25 30  
Ala Asn Ser Gly Asp Pro Asn  
35

30

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Glu Trp Tyr Ser Trp Lys Arg Ser Ser Lys Ser Thr Gly Leu Gly Asp  
 1 5 10 15  
 Thr Ala Thr Arg Glu Gly Cys Gly Pro Ser Gln Ser Asp Gly Cys Pro  
 20 25 30  
 Tyr Asn Gly Arg Leu Thr Thr Val Lys Pro Arg Lys  
 35 40

5 (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp  
 1 5 10 15  
 Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val  
 20 25 30  
 Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu  
 35 40

15 (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys Glu  
 1 5 10 15  
 Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg Lys  
 20 25 30  
 Val Phe Asn Arg Arg Arg Pro Ser Ala Ile Pro Thr  
 35 40

25 (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Arg His Ile Ser Glu Tyr Ser Phe Ala Asn Ser His Leu Met Gly Gly  
 1 5 10 15  
 Glu Ser Lys Arg Lys Gly Cys Gly Ile Asn Gly Ser Phe Ser Pro Thr  
 20 25 30  
 Cys Pro Arg Ser Pro Thr Pro Ala Phe Arg Arg Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:54:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ser Arg Glu Ser Gly Met Trp Gly Ser Trp Trp Arg Gly His Arg Leu  
1 5 10 15  
Asn Ser Thr Gly Gly Asn Ala Asn Met Asn Ala Ser Leu Pro Pro Asp  
20 25 30  
Pro Pro Val Ser Thr Pro  
35

10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
1 5 10 15  
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu  
20 25 30  
Arg Thr Arg Ser Arg Pro Asn  
35

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TCTCACTCCT CGAGATCCGG CGCTTATGAG AGTCCGGATG GTCGGGGGGG TCGGAGCTAT 60  
GTGGGGGGCG GGGGTGGNTG TGGTAACATT GGTCGGAAGC ATAACCTGTG GGGGCTGCGT 120  
ACCGCGTCGC CGGCCTGCTG GGA CTCTAGA ATCGAAGTC GCGCTAGACC TTCGAGA 177

30

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCTCACTCCT CGAGTCCTCG CTCTTCTGG CCCGTTGTGT CCCGGCATGA GTCGTTTGGG 60  
ATCTCTAACT ATTGGGNTG TGGTTATCGT ACATGTATCT CCGGCACGAT GACTAAGTCT 120

AGCCCCGATT ACCCTCGGCA TTCGTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA

177

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCTCACTCCT	CGAGTAGTAG	CTCCGATTGG	GGTGGTGTGC	CTGGGAAGGT	GGTTAGGGAG	60
CGCTTTAAGG	GGCGCGGTTG	TGGTATTTCC	ATCACCTCCG	TGCTCACTGG	GAAGCCCAAT	120
CCGTGTCCGG	AGCCTAAGGC	GGCCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TCTCACTCCT	CGAGAGTTGG	CCAGTGCACG	GATTCTGATG	TGCGGCGTCC	TTGGGCCAGG	60
TCTTGCGCTC	ATCAGGGTTG	TGGTGCGGGC	ACTCGCAACT	CGCACGGCTG	CATCACCCTG	120
CCTCTCCGCC	AGGCTAGCGC	TCATTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCTCACTCCT	CGAGCCACTC	CGGTGGTATG	AATAGGGCCT	ACGGGGATGT	GTTTAGGGAG	60
CTTCGTGATC	GGTGAACGC	CACTTCCCAC	CACACTCGCC	CCACCCCTCA	GCTCCCCCGT	120
GGGCCTAATT	CTAGAATCGA	AGGTGCGGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCTCACTCCT	CGAGTCCGTG	CGGGGGGTG	TGGGGGCGTT	TTATGCAGGG	TGGCCTTTTC	60
GGCGGTAGGA	CTGATGGTTG	TGGTGCCCAT	AGAAACCGCA	CTTCTGCGTC	GTTAGAGCCC	120
CCGAGCAGCG	ACTACTCTAG	AATCGAAGGT	GCGCTAGAC	CTTCGAGA		168

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTCACTCCT	CGAGGGGCGC	CGCCGATCAG	CGGCGGGGGT	GGTCCGAGAA	CTTGGGGTTG	60
CCTAGGGTGG	GGTGGGACGC	CATCGCTCAC	AATAGCTATA	CGTTCACCTC	GCGCCGCCCCG	120
CGCCCCCCT	CTAGA					135

10

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TCTCACTCCT	CGAGCGGTGG	GGAGGTCAGC	TCCTGGGGCC	GCGTGAATGA	CCTCTGCGCT	60
AGGGTGAGTT	GGACTGGTTG	TGGTACTGCT	CGTTCCGCGC	GTACCGACAA	CRAAGGCTTT	120
CTTCCTAAGC	ACTCGTCACT	CCGCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:64:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

25

TCTCACTCCT	CGAGTGATAG	TGACGGGGAT	CATTATGGGC	TTGCGGGGGG	GGTGCGTTGT	60
TCGCTTCGTG	ATAGGGGTG	TGGTCTGGCC	CTGTCCACCG	TCCATGCTGG	TCCCCCTCT	120
TTTTACCCA	AGCTCTCCAG	CCCCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

35

TCTCACTCCT	CGAGGAGCTT	GGGTAATTAT	GGCGTCACCG	GGACTGTGGA	CGTGACGGTT	60
TTGCCCATGC	CTGGCCACGC	CAACCACTT	GGTGTCTCCT	CCGCCTCTAG	CTCTGATCCT	120
CCGCGGCGCT	CTAGAATCGA	AGGTGCGGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 bas pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTCACTCCT	CGAGAACTAC	GACGGCTAAG	GGGTGTCTTC	TCGGAAGCTT	CGGCGTTCTT	60
AGTGGGTGCT	CATTACGCC	AACCTCTCCA	CGCCCCACC	TAGGATACCC	CCCCCACTCC	120
GTCAATTCTA	GAATCGAAG	TCGCGCTAGA	CCTTCGAGA			159

(2) INFORMATION FOR SEQ ID NO:67:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

15

TCTCACTCCT	CGAGCCCGAA	GTTGTCCAGC	GTGGGTGTTA	TGACTAAGGT	CACGGAGCTG	60
CCCACGGAGG	GGCCTAACGC	CATTAGTATT	CCGATCTCCG	CGACCCCTCG	CCCGCGCAAC	120
CCGCTCCGCT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TCTCACTCCT	CGAGGTGGTG	CGGCGCTGAG	CTGTGCAACT	CGGTGACTAA	GAAGTTTCGC	60
CCGGGCTGGC	GGGATCACGC	CAATCCCTCC	ACCCATCATC	GTACTCCCCC	GCCCAGCCAG	120
TCCAGCCCTT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TCTCACTCCT	CGAGGTGGTG	CGGCGCTGAT	GACCCGTGTG	GTGCCAGTCG	TTGGCGGGGG	60
GGCAACAGCT	TGTTTGTTG	TGGTCTTCGT	TGTAGTGGG	CGCAGAGCAC	CCCGAGTGGC	120
AGGATCCATT	CCACTTCGAC	CAGCTCTAGA	ATCGAAGGTG	CGCTAGACCT	TCGAGA	176

35

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs

(B) TYPE: nucl ic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

5 TCTCACTCCT CGAGTAAGTC CGGGGAGGGG GGTGACAGTA GCAGGGGCGA GACGGGCTGG 60  
GCGAGGGTTC GGTCTCACGC CATGACTGCT GGCCGCTTTC GGTGGTACAA CCAGTTGCCC 120  
TCTGATCGGT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

15 TCTCACTCCT CGAGGTCGAG CGCCAATAAT TCGAGTGGA AGTCTGATTG GATGCGCAGG 60  
GCCTGTATTG CTCGTTACGC CAACAGTTCG GGCCCCGCCC GCGCCGTCGA CACTAAGGCC 120  
GCGCCCTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

25 TCTCACTCCT CGAGTAAGTG GTCGTGGAGT TCGAGGTGGG GCTCCCCGCA GGATAAGGTT 60  
GAGAAGACCA GGGCGGGTTG TGGTGGTAGT CCCAGCAGCA CCAATTGTCA CCCCTACACC 120  
TTTGCCCCC CCGCGCAGC CGGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TCTCACTCCT CGAGTGGGTT CTGGGAGTTT ACCAGGGGGC TTTGGGATGG GGAGAACCGT 60  
AAGAGTGTCC GGTGCGGTTG TGGTTTTCTG GGCTCCTCTG CTCAGGGCCC GTGTCCGGTC 120  
ACGCCTGCCA CCATTGACAA ACACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:74:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

5 TCTCACTCCT CGAGTGAGAG CGGGCGGTGC CGTAGCGTGA GCCGGTGGAT GACGACGTGG 60  
CAGACGCAGA AGGGCGGTTG TGGTTCCAAT GTTTCCCGCG GTTCGCCCCT CGACCCCTCT 120  
CACCAGACCG GGCATGCCAC TACTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

15 TCTCACTCCT CGAGGGAGTG GAGGTTTGCC GGGCCCGCGT TGGACCTGTG GGCGGGTCCG 60  
AGCTTGCCCT CTTTAAACGC CAGTCCCAC CCTCGCGCCC TCGCACCTA TTGGTCCCAG 120  
CGGCCCCGCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TCTCACTCCT CGAGGATGGA GGACATCAAG AACTCGGGGT GGAGGGACTC TTGTAGGTGG 60  
GGTGACCTGA GGCCTGGTTG TGGTAGCCGC CAGTGGTACC CCTCGAATAT GCGTTCTAGC 120  
AGAGATTACC CCGCGGGGGG CCACTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:77:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCTCACTCCT CGAGTCATCC GTGGTACAGG CATTGGAACC ATGGTGACTT CTCTGGTTCG 60  
GGCCAGTCAC GCCACACCCC GCCGGAGAGC CCCACCCCG GCCGCCCTAA TGCCACCATT 120  
TCTAGAATCG AAGGTCGCGC TAGACCTTCG AG 152

(2) INFORMATION FOR SEQ ID NO:78:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TCTCACTCCT	CGAGATATAA	GCACGATATC	GGTTGCGATG	CTGGGGTTGA	CAAGAAGTCG	60
TCGTCTGTGC	GTGGTGGTTG	TGGTGCTCAT	TNGTCGCCAC	CCCGCGCCGG	CCGTGGTCCT	120
CGCGGCACGA	TGTTAGCAG	GCTTTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCTCACTCCT	CGAGTCAGGG	CTCCAAGCAG	TGTATGCAGT	ACCGCACCGG	TCGTTTGACG	60
GTGGGGTCTG	AGTATGGTTG	TGGTATGAAC	CCCGCCCGCC	ATGCCACGCC	CGCTTATCCG	120
GCGCGCCTGC	TGCCACGCTA	TCGCTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:80:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCTCACTCCT	CGAGTGGGCG	GACTIONAGT	GAGATTCTG	GGCTCTGGGG	TTGGGGTGAC	60
GACCGGAGCG	GTTATGGTTG	GGGTAAACAG	CTCCGCCCCA	ACTACATCCC	TTATAGGCAG	120
GCGACGAACA	GGCATCGTTA	TACGTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTCACTCCT	CGAGGTGGAA	TTGGACTGTC	TTGCCCGCCA	CTGGCGGCCA	TTACTGGACG	60
CGTTGACGCG	ACTATCACGC	CATTAAACAT	CACAGGCCGA	GATCCCCCA	CCAGCATCCG	120
ACCCCTATCT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCTCACTCCT	CGAGTTGGTC	GTCTGGAAT	TGGAGCTCTA	AGACTACTCG	TCTGGGCGAC	60
AGGGCGACTC	GGGAGGGTTG	TGGTCCCAGC	CAGTCTGATG	GCTGTCCTTA	TAACGGCCGC	120
CTTACGACCG	TCAAGCCTCG	CACGTCTAGA	ATCGAAGGTC	GCGCTAGACC	TCGAGA	177

(2) INFORMATION FOR SEQ ID NO:83:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TCTCACTCCT	CGAGTGGTAG	TTTGAACGCA	TGGCAACCGC	GGTCATGGGT	GGGGGGCGCG	60
TTCCGGTCAC	ACGCCAACAA	TAAGTTGAAC	CCCAAGCCCA	CCATGGTTAC	TNGTCACCCT	120
ACCTCTAGAA	TCGAAGGTCG	CGCTAGACCT	TCGAGA			156

(2) INFORMATION FOR SEQ ID NO:84:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCTCACTCCT	CGAGGTATTC	GGGTTTGTC	CCGCGGGACA	ACGGTCCCGC	TTGTAGTCAG	60
GAGGCTACCT	TGGAGGGTTG	TGGTGCGCAG	AGGCTGATGT	CCACCCGTCG	CAAGGGCCGC	120
AACTCCCGCC	CCGGGTGGAC	GCTCTCTAGA	ATCGAAGGTC	GCGCTAGACC	CTTCGAGA	178

(2) INFORMATION FOR SEQ ID NO:85:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TCTCACTCCT	CGAGCGTGGG	GAATGATAAG	ACTAGCAGGC	CGGTTTCCTT	CTACGGGCGC	60
GTTAGTGATC	TGTGGAACGC	CAGCTTGATG	CCGAAGCGTA	CTCCAGCTC	GAAGCGCCAC	120
GATGATGGCT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

30

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:



TCTCACTCCT CGAGTACTCC CCCAGTAGG GAGGCGTATA GTAGGCCCTA TAGTGTGAT 60  
 AGCGATTCGG ATACGAACGC CAAGCACAGC TCCCACAACC GCCGTNTGCG GACGCGCAGC 120  
 CGCCCGAACT CTAGAATCGA AGGTGCGGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:87:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

10 TCTCACTCCT CGAGATGGCC TAGTGTGGGT TACAAGGTA ATGGCAGTGA CACTATTGAT 60  
 GTTCACAGCA ATGACGCCAG TACTAAGAGG TCCCTCATCT ATAACCACCG CCGCCCCNTC 120  
 TTTCCCTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAGA 159

(2) INFORMATION FOR SEQ ID NO:88:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

20 TCTCACTCCT CGAGAACGTT TGAGAACGAC GGGCTGGGCG TCGGCCGGTC TATTCAGAAG 60  
 AAGTCGGATA GGTGGTACGC CAGCCACAAC ATTCTAGCC ATTCGCGTC CATGTCTCCC 120  
 GCTGGTAAGT CTAGAATCGA AGGTGCGGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:89:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

30 TCTCACTCCT CGAGCTATTG TCGGGTTAAG GGTGCTGGG AGGGGGGGCA TACGGATTCC 60  
 AATCTGGCTA GGTGCGGTTG TGGTAAGGTG GCCAGGACCA GCAGGCTTCA GCATATCAAC 120  
 CCGCGCGCTA CCCCCCCTC CCGGTCTAGA ATCGAAGGTC 160

(2) INFORMATION FOR SEQ ID NO:90:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TCTCACTCCT CGAGTTGGAC TCGGTGGGGC AAGCACANTC ATGGGGGGTT TGTGAACAAG 60  
 TCTCCCCCTG GGAAGAACGC CACGAGCCCC TACACCGACG CCCAGCTGCC CAGTGATCAG 120

GGTCCTCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA

162

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

10 TCTCACTCCT CGAGTCAGGT TGATTCGTTT CGTAATAGCT TTCGGTGGTA TGAGCCGAGC 60  
AGGGCTCTGT GCCATGGTTG TGGTAAGCGC GACACCTCCA CCACTCGTAT CCACAATAGC 120  
CCCAGCGACT CCTATCCTAC ACGCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TCTCACTCCT CGAGCTTTTT GCGGTTCCAG AGTCGAGGT TCGAGGATTA CAGTAGGACG 60  
ATCTNTCGGT TGC GCAACGC CACGAACCG AGTAATGTCT CCGATGCGCA CAATAACCGG 120  
GCCTTGGCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TCTCACTCCT CGAGGAGCAT CACCGACGGG GGCATCAATG AGGTGGACCT GAGTAGTGTG 60  
TCGAACGTTT TCGAAGCGC CAACTCGCAT AGGGCCTACA GGAAGCATCG CCCGACCTTG 120  
AAGCGTCCTT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:94:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

35

TCTCACTCCT CGAGTTTCGAA GGTGAGCAGC CCGAGGGATC CGACGGTCCC GCGGAAGGGC 60  
GGCAATGTTG ATTATGGTTG TGGTCACAGG TCTTCGCCCC GGATGCCTAC CTCCGCTCTG 120  
TCGTGATCA CGAAGTGCTA CACTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTCACTCCT	CGAGAGCCAG	TANGCAGGGC	GGCCGGGGTG	TTGCCCTGA	TTTGGGGCG	60
AGCGTTTTGG	GTNGTGGTTG	TGGTAGCGCC	ACTTATTACA	CGAACTCCAC	CAGCTGCAAG	120
GATGCTATGG	GCCACAATA	CTCGTCTAGA	ATCGAAGGTC	GCGNTAGACC	TTCGAGA	177

10

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCTCACTCCT	CGAGATGGTG	CGAGAAGCAC	AAGTTACGG	CTGCGCGTTG	CAGCGCGGGG	60
GCGGGTTTTG	AGAGGGANGC	CAGCCGTCCG	CCCCAGCCTG	CCCACCGGGA	TAATACCAAC	120
CGTAATGCNT	NTAGAATCGA	AGGTGCGGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:97:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

25

TCTCACTCCT	CGAGTTTTCA	GGTGTACCCG	GACCATGGTC	TGGAGAGGCA	TGCTTTGGAC	60
GGGACGGGTC	CGCTTTACGC	CATGCCCGGC	CGCTGGATTA	GGGCGCGTCC	GCAGAACAGG	120
GACCGCCAGT	CTAGAATCGA	AGGTGCGGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TCTCACTCCT	CGAGCAGGTG	TACGGACAAC	GAGCAGTGCC	CCGATACCGG	GANTAGGTCT	60
CGTTCCGTTA	GTAACGCCAG	GTACTTTTCG	AGCAGGTTGC	TCAAGACTCA	CGCCCCCAT	120
CGCCCTTCTA	GAATCGAAGG	TCGCGCTAGA	CCTTCGAGA			159

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTCACTCCT	CGAGTGCCAG	GGATAGCGGG	CCTGCGGAGG	ATGGGTCCCG	CGCCGTCCGG	60
TTGAACGGGG	TTGAGAACGC	CAACACTAGG	AAGTCCTCCC	GCAGTAACCC	GCGGGGTAGG	120
CGCCATCCCT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:100:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

15

TCTCACTCCT	CGAGTTCCGC	CGATCGGAG	AAGTGTGCGG	GCAGTCTGTT	GTGGTGGGGT	60
AGGCAGAAC	ACTCCGGTTG	TGGTTCGCCC	ACGAAGAAGC	ATCTGAAGCA	CCGCAATCGC	120
AGTCAGACCT	CCTCTTCGTC	CACTCTAGA	ATCGAAGGTC	GCGCTAGACC	TTCGAGA	177

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTCACTCCT	CGAGACCGAA	GAACGTGGCC	GATGCTTATT	CGTCTCAGGA	CGGGGCGGCG	60
GCCGAGGAGA	CGTCTCACGC	CAGTAATGCC	GCGCGGAAGT	CCCCTAAGCA	CAAGCCCTTG	120
AGGCGGCCTT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TCTCACTCCT	CGAGAGGCAG	TACGGGGACG	GCCGGCGGCG	AGCGTTCCGG	GGTGCTCAAC	60
CTGCACACCA	GGGATAACGC	CAGCGGCAGC	GGTTTCAAAC	CGTGGTACCC	TTCGAATCGG	120
GGTCACAAGT	CTAGAATCGA	AGGTCGCGCT	AGACCTTCGA	GA		162

35

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

5 TCTCACTCCT CGAGGTGGGG GTGGGAGAGG AGTCCGTCCG ACTACGATTG TGATATGGAC 60  
 TTGGGGGCGA GGAGGTACGC CACCCGCACC CACCGCGCGC CCCCTCGCGT CTTGAAGGCT 120  
 CCCCTGCCCT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

15 TCTCACTCCT CGAGGCACTG GAAGTGCAGG GGCTCTCAGG CTGCCTACGG GGACAAGGAT 60  
 ATCGGGAGGT CCAGGGGTTG TGGTCCATT ACAAAGAATA AACTAATCA CGCCCATCCT 120  
 AGCCACGGCG CCGTTGCTAA GATCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

20 TCTCACTCCT CGAGCCGCGA GGAGGCCAAC TGGGACGGCT ATAAGAGGGA GATGAGCCAC 60  
 CGGAGTCGCT TTTGGGACGC CACCCACCTG TCCCGCCCTC GCGCCCCGC TAACTCTGCT 120  
 GACCCTAACT CTAGAATCGA AGGTCGCGCT AGACCTTCGA GA 162

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

30 TCTCACTCNT CGAGAGAGTT CGCGGAGAGG AGGTTGTGGG GGTGTGATGA CCTGAGTTGG 60  
 CGTCTCGACG CGGAGGGTTG TGGTCCCACT CCGAGCAATC GGGCCGTCAA GCATCGCAAG 120  
 CCGCCCCAC GCTCCCCCGC ACTCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

5 TCTCACTCNT NGAGTGATCA CGCGTTGGGG ACGAATCTGA GGTCTGACAA TGCCAAGGAG 60  
CCGGGTGATT ACAACTGTTG TGGTAACGGG AACTCTACCG GCGGAAAGGT TTTTAACCGT 120  
AGGCGCCCCT CCGCCATCCC CANTTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

15 TCTCACTCCT CGAGGCATAT TTCTGAGTAT AGCTTTGCGA ATTCCCACTT GATGGGTGGC 60  
GAGTCCAAGC GGAAGGGTTG TGGTATTAAC GGCTCCTTTT CTCCCACTTG TCCCGCTCC 120  
CCCACCCCAG CCTTCCGCCG CACCTCTAGA ATCGAAGGTC GCGCTAGACC TTCGAGA 177

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCTCACTCCT CGAGCCGGGA GAGCGGGATG TGGGGTAGTT GGTGGCGTGG TCACAGGTTG 60  
AATCCACGG GGGGTAACGC CAACATGAAT GCTAGTCTGC CCCCCGACCC CCCTGTTCC 120  
ACTCCGTCTA GAATCGAAGG TCGCGCTAGA CCTTCGAG 158

(2) INFORMATION FOR SEQ ID NO:110:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile  
1 5 10 15  
Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly  
20 25 30  
Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp  
35 40 45  
Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr  
50 55 60  
Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys  
65 70 75 80  
Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala  
85 90 95

Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp  
 100 105 110  
 Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly  
 115 120 125  
 Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser  
 130 135 140  
 Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn  
 145 150 155  
 5 Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu  
 165 170 175  
 Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His  
 180 185 190  
 Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu  
 195 200 205  
 Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys  
 210 215 220  
 10 Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile  
 225 230 235 240  
 Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro  
 245 250 255  
 Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg  
 260 265 270  
 Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile  
 275 280 285  
 Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp  
 290 295 300  
 15 Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile  
 305 310 315 320  
 Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met  
 325 330 335  
 Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly  
 340 345 350  
 Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala  
 355 360 365  
 20 Ser Met Ala Phe Val Val Ala Ile Val Gln Val Glu Ile Asp Lys  
 370 375 380  
 Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu  
 385 390 395 400  
 Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val  
 405 410 415  
 Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val  
 420 425 430  
 Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr  
 435 440 445  
 25 Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val  
 450 455 460  
 Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys  
 465 470 475 480  
 Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu  
 485 490 495  
 Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser  
 500 505 510  
 30 Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe  
 515 520 525  
 Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn  
 530 535 540  
 Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg  
 545 550 555 560  
 Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala  
 565 570 575  
 Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr  
 580 585 590  
 35 Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser  
 595 600 605  
 Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu  
 610 615 620

Thr Val Ala Val Gly Asn Ile Ile Val Leu Il Val Ala Gly Ala Gly  
 625 630 635 640  
 Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu  
 645 650 655  
 Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr  
 660 665 670  
 Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys  
 675 680 685  
 5 Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser  
 690 695 700  
 Gln Lys Gln Met  
 705

(2) INFORMATION FOR SEQ ID NO:111:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

15 TCCGGACTCT CATAAGCGCC GG

22

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ACAACGGGCC AGAAAGAGCG AG

22

(2) INFORMATION FOR SEQ ID NO:113:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

30

ACACCACCCC AATCGGAGCT AC

22

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:



TCAGAATCCG TGCACTGGCC AA

22

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCCCTATTCA TACCACCGGA GT

22

10

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CATCAGTCCT ACCGCCGAAA AG

22

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGTATAGCTA TTGTGAGCGA TG

22

25

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACGCGCGGAA CGAGCAGTAC CA

22

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCATAATGAT CCCCCTCACT AT 22

(2) INFORMATION FOR SEQ ID NO:120:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

AGACACCCCT TAGCCGTCGT AG 22

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

AGCTCCGTGA CCTTAGTCAT AA 22

(2) INFORMATION FOR SEQ ID NO:122:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TGCACAGCTC AGCGCCGCAC CA 22

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

30 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ACGGGTCATC AGCGCCGCAC CA 22

(2) INFORMATION FOR SEQ ID NO:124:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

5 TGTCACCCCC CTCCCCGGAC TT

22

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTCGCAATT ATTGGCGCTC GA

22

(2) INFORMATION FOR SEQ ID NO:126:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GTCTTCTCAA CCTTATCCTG CG

22

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AAAGCCCCCT GCTAAACTCC CA

22

(2) INFORMATION FOR SEQ ID NO:128:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCGTCTGC CACGTCGTCA TC

22

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GTAAAAGAG GGCAAGCTCG GA 22

(2) INFORMATION FOR SEQ ID NO:130:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

15 CCGAGTTCTT GATGTCCTCC AT 22

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TCCAATGCCT GTACCACGGA TG 22

(2) INFORMATION FOR SEQ ID NO:132:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

30 TCGCAACCGA TATCGTGCTT AT 22

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:  
TGCATACACT GCTTGGAGCC CT 22

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:  
5 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:  
10 GAAATCTCAC TAGTAGTCCG CC 22

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:  
GCGGGCAAGA CAGTCCAATT CC 22

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:  
25 GAGCTCCAAT TCCACGACGA CC 22

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:  
GGTTGCCATG CGTTCAAAC AC 22

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

5 TCCCGCGGGG ACAAACCCGA AT 22

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CTGCTAGTCT TATCATTCCC CA 22

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

20 CTATCGACAC TATAGGGCCT AC 22

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

TACCCTTGTA ACCCACACTA GG 22

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

35 TTCTTCTGAA TAGACCGGCC GA 22

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:  
 CCACCACCCT TAACCCGACA AT 22

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:  
 AGGGGGAGAC TTGTTCAACA AC 22

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:  
 CGGCTCATAC CACCGAAAGC TA 22

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:  
 ATCGTCCTAC TGTAATCCTC GA 22

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:  
 ATCGTCCTAC TGTAATCCTC GA 22

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:  
 ATCGTCCTAC TGTAATCCTC GA 22

GACACACTAC TCAGGTCCAC CT

22

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

CCATAATCAA CATTGCCGCC CT

22

(2) INFORMATION FOR SEQ ID NO:149:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CAAAACGCTC GCCCCAAACT CA

22

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTAAACTGT GCTTCTCGCA CC

22

25

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CCATGGTCCG GGTACACCTG AA

22

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:  
 GTTACTAACG GAACGAGACC TA 22

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
 5 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:  
 10 TGTTGGCGTT CTCAACCCCG TT 22

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:  
 ACAACCGGAG TTGTTCTGCC TA 22

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:  
 25 TAAGCATCGG CCACGTTCTT CG 22

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:  
 TTATCCCTGG TGTGCAGGTT GA 22

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TATCAGAATC GTAGTCGGAC GG 22

5 (2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTTTGTAATG GAACCACAAC CC 22

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

20 CGGTGGCTCA TCTCCCTCTT AT 22

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATCAGACTGG CTGGGACCAC AA 22

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

35 CACAACCTCC TCTCCGCGAA CT 22

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: singl  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:  
 AGATTCGTCC CCAACGCGTG AT 22

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:  
 GGGAATTCGC AAAGCTATAC TC 22

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:  
 CCCCCTGGAA TTCAACCTGT GA 22

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:  
 30 GTCGTCTTTC CAGACGT 17

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

## (2) INFORMATION FOR SEQ ID NO:167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala Phe Glu  
 1 5 10 15  
 10 Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln Leu Ser  
 20 25 30  
 Phe Thr Pro Glu Glu  
 35

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Arg Glu Phe Ala Glu Arg Arg Leu Trp Gly Cys Asp Asp Leu Ser Trp  
 1 5 10 15  
 20 Arg Leu Asp Ala Glu Gly Cys Gly Pro Thr Pro Ser Asn Arg Ala Val  
 25 30  
 Lys His Arg Lys Pro Arg Pro Arg Ser Pro Ala Leu  
 35 40

## (2) INFORMATION FOR SEQ ID NO:169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Ser Gly Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe  
 1 5 10 15  
 Arg Glu Leu Arg Asp Arg Trp Tyr Ala Thr Ser His His Thr Arg Pro  
 20 25 30  
 Thr Pro Gln Leu Pro Arg Gly Pro Asn  
 35 40

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
1 5 10 15  
Ser Asp Ser Asp  
20

5

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
1 5 10 15  
Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn  
20 25

15

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser  
1 5 10 15  
Arg Pro Asn

25

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Thr Asn Ala Lys His Ser Ser His Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
1 5 10

5 (2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

20 Met Gly Met Ser Lys Ser His Ser Phe Phe Gly Tyr Pro Leu Ser Ile  
1 5 10 15  
Phe Phe Ile Val Val Asn Glu Phe Cys Glu Arg Phe Ser Tyr Tyr Gly  
20 25 30  
Met Arg Ala Ile Leu Ile Leu Tyr Phe Thr Asn Phe Ile Ser Trp Asp  
35 40 45  
Asp Asn Leu Ser Thr Ala Ile Tyr His Thr Phe Val Ala Leu Cys Tyr  
50 55 60  
Leu Thr Pro Ile Leu Gly Ala Leu Ile Ala Asp Ser Trp Leu Gly Lys  
65 70 75 80  
25 Phe Lys Thr Ile Val Ser Leu Ser Ile Val Tyr Thr Ile Gly Gln Ala  
85 90 95  
Val Thr Ser Val Ser Ser Ile Asn Asp Leu Thr Asp His Asn His Asp  
100 105 110  
Gly Thr Pro Asp Ser Leu Pro Val His Val Val Leu Ser Leu Ile Gly  
115 120 125  
Leu Ala Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser  
130 135 140  
30 Ala Phe Gly Gly Asp Gln Phe Glu Glu Gly Gln Glu Lys Gln Arg Asn  
145 150 155 160  
Arg Phe Phe Ser Ile Phe Tyr Leu Ala Ile Asn Ala Gly Ser Leu Leu  
165 170 175  
Ser Thr Ile Ile Thr Pro Met Leu Arg Val Gln Gln Cys Gly Ile His  
180 185 190  
Ser Lys Gln Ala Cys Tyr Pro Leu Ala Phe Gly Val Pro Ala Ala Leu  
195 200 205  
Met Ala Val Ala Leu Ile Val Phe Val Leu Gly Ser Gly Met Tyr Lys  
210 215 220  
35 Lys Phe Lys Pro Gln Gly Asn Ile Met Gly Lys Val Ala Lys Cys Ile  
225 230 235 240  
Gly Phe Ala Ile Lys Asn Arg Phe Arg His Arg Ser Lys Ala Phe Pro  
245 250 255

Lys Arg Glu His Trp Leu Asp Trp Ala Lys Glu Lys Tyr Asp Glu Arg  
 260 265 270  
 Leu Ile Ser Gln Ile Lys Met Val Thr Arg Val Met Phe Leu Tyr Ile  
 275 280 285  
 Pro Leu Pro Met Phe Trp Ala Leu Phe Asp Gln Gln Gly Ser Arg Trp  
 290 295 300  
 Thr Leu Gln Ala Thr Thr Met Ser Gly Lys Ile Gly Ala Leu Glu Ile  
 305 310 315  
 5 Gln Pro Asp Gln Met Gln Thr Val Asn Ala Ile Leu Ile Val Ile Met  
 325 330 335  
 Val Pro Ile Phe Asp Ala Val Leu Tyr Pro Leu Ile Ala Lys Cys Gly  
 340 345 350  
 Phe Asn Phe Thr Ser Leu Lys Lys Met Ala Val Gly Met Val Leu Ala  
 355 360 365  
 Ser Met Ala Phe Val Val Ala Ala Ile Val Gln Val Glu Ile Asp Lys  
 370 375 380  
 10 Thr Leu Pro Val Phe Pro Lys Gly Asn Glu Val Gln Ile Lys Val Leu  
 385 390 395 400  
 Asn Ile Gly Asn Asn Thr Met Asn Ile Ser Leu Pro Gly Glu Met Val  
 405 410 415  
 Thr Leu Gly Pro Met Ser Gln Thr Asn Ala Phe Met Thr Phe Asp Val  
 420 425 430  
 Asn Lys Leu Thr Arg Ile Asn Ile Ser Ser Pro Gly Ser Pro Val Thr  
 435 440 445  
 Ala Val Thr Asp Asp Phe Lys Gln Gly Gln Arg His Thr Leu Leu Val  
 450 455 460  
 15 Trp Ala Pro Asn His Tyr Gln Val Val Lys Asp Gly Leu Asn Gln Lys  
 465 470 475 480  
 Pro Glu Lys Gly Glu Asn Gly Ile Arg Phe Val Asn Thr Phe Asn Glu  
 485 490 495  
 Leu Ile Thr Ile Thr Met Ser Gly Lys Val Tyr Ala Asn Ile Ser Ser  
 500 505 510  
 Tyr Asn Ala Ser Thr Tyr Gln Phe Phe Pro Ser Gly Ile Lys Gly Phe  
 515 520 525  
 20 Thr Ile Ser Ser Thr Glu Ile Pro Pro Gln Cys Gln Pro Asn Phe Asn  
 530 535 540  
 Thr Phe Tyr Leu Glu Phe Gly Ser Ala Tyr Thr Tyr Ile Val Gln Arg  
 545 550 555 560  
 Lys Asn Asp Ser Cys Pro Glu Val Lys Val Phe Glu Asp Ile Ser Ala  
 565 570 575  
 Asn Thr Val Asn Met Ala Leu Gln Ile Pro Gln Tyr Phe Leu Leu Thr  
 580 585 590  
 Cys Gly Glu Val Val Phe Ser Val Thr Gly Leu Glu Phe Ser Tyr Ser  
 595 600 605  
 25 Gln Ala Pro Ser Asn Met Lys Ser Val Leu Gln Ala Gly Trp Leu Leu  
 610 615 620  
 Thr Val Ala Val Gly Asn Ile Ile Val Leu Ile Val Ala Gly Ala Gly  
 625 630 635 640  
 Gln Phe Ser Lys Gln Trp Ala Glu Tyr Ile Leu Phe Ala Ala Leu Leu  
 645 650 655  
 Leu Val Val Cys Val Val Phe Ala Ile Met Ala Arg Phe Tyr Thr Tyr  
 660 665 670  
 30 Ile Asn Pro Ala Glu Ile Glu Ala Gln Phe Asp Glu Asp Glu Lys Lys  
 675 680 685  
 Asn Arg Leu Glu Lys Ser Asn Pro Tyr Phe Met Ser Gly Ala Asn Ser  
 690 695 700  
 Gln Lys Gln Met  
 705

(2) INFORMATION FOR SEQ ID NO:177:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3345 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding S quence  
(B) LOCATION: 88...2583  
(D) OTHER INFORMATION:

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

	GAATTCGTC TCGACCACTG AATGGAAGAA AAGGACTTTT AACCAACCATT TTGTGACTTA	60
	CAGAAAGGAA TTTGAATAAA GAAACT ATG ATA CTT CAG GCC CAT CTT CAC TCC	114
	Met Ile Leu Gln Ala His Leu His Ser	
	1 5	
10	CTG TGT CTT CTT ATG CTT TAT TTG GCA ACT GGA TAT GGC CAA GAG GGG	162
	Leu Cys Leu Leu Met Leu Tyr Leu Ala Thr Gly Tyr Gly Gln Glu Gly	
	10 15 20 25	
	AAG TTT AGT GGA CCC CTG AAA CCC ATG ACA TTT TCT ATT TAT GAA GGC	210
	Lys Phe Ser Gly Pro Leu Lys Pro Met Thr Phe Ser Ile Tyr Glu Gly	
	30 35 40	
15	CAA GAA CCG AGT CAA ATT ATA TTC CAG TTT AAG GCC AAT CCT CCT GCT	258
	Gln Glu Pro Ser Gln Ile Ile Phe Gln Phe Lys Ala Asn Pro Pro Ala	
	45 50 55	
	GTG ACT TTT GAA CTA ACT GGG GAG ACA GAC AAC ATA TTT GTG ATA GAA	306
	Val Thr Phe Glu Leu Thr Gly Glu Thr Asp Asn Ile Phe Val Ile Glu	
	60 65 70	
	CGG GAG GGA CTT CTG TAT TAC AAC AGA GCC TTG GAC AGG GAA ACA AGA	354
	Arg Glu Gly Leu Leu Tyr Tyr Asn Arg Ala Leu Asp Arg Glu Thr Arg	
	75 80 85	
20	TCT ACT CAC AAT CTC CAG GTT GCA GCC CTG GAC GCT AAT GGA ATT ATA	402
	Ser Thr His Asn Leu Gln Val Ala Ala Leu Asp Ala Asn Gly Ile Ile	
	90 95 100 105	
	GTG GAG GGT CCA GTC CCT ATC ACC ATA GAA GTG AAG GAC ATC AAC GAC	450
	Val Glu Gly Pro Val Pro Ile Thr Ile Glu Val Lys Asp Ile Asn Asp	
	110 115 120	
25	AAT CGA CCC ACG TTT CTC CAG TCA AAG TAC GAA GGC TCA GTA AGG CAG	498
	Asn Arg Pro Thr Phe Leu Gln Ser Lys Tyr Glu Gly Ser Val Arg Gln	
	125 130 135	
	AAC TCT CGC CCA GGA AAG CCC TTC TTG TAT GTC AAT GCC ACA GAC CTG	546
	Asn Ser Arg Pro Gly Lys Pro Phe Leu Tyr Val Asn Ala Thr Asp Leu	
	140 145 150	
30	GAT GAT CCG GCC ACT CCC AAT GGC CAG CTT TAT TAC CAG ATT GTC ATC	594
	Asp Asp Pro Ala Thr Pro Asn Gly Gln Leu Tyr Tyr Gln Ile Val Ile	
	155 160 165	
	CAG CTT CCC ATG ATC AAC AAT GTC ATG TAC TTT CAG ATC AAC AAC AAA	642
	Gln Leu Pro Met Ile Asn Asn Val Met Tyr Phe Gln Ile Asn Asn Lys	
	170 175 180 185	
35	ACG GGA GCC ATC TCT CTT ACC CGA GAG GGA TCT CAG GAA TTG AAT CCT	690
	Thr Gly Ala Ile Ser Leu Thr Arg Glu Gly Ser Gln Glu Leu Asn Pro	
	190 195 200	
	GCT AAG AAT CCT TCC TAT AAT CTG GTG ATC TCA GTG AAG GAC ATG GGA	738
	Ala Lys Asn Pro Ser Tyr Asn Leu Val Ile Ser Val Lys Asp Met Gly	
	205 210 215	



	GGC CAG AGT GAG AAT TCC TTC AGT GAT ACC ACA TCT GTG GAT ATC ATA	786
	Gly Gln Ser Glu Asn Ser Phe Ser Asp Thr Thr Ser Val Asp Ile Ile	
	220 225 230	
	GTG ACA GAG AAT ATT TGG AAA GCA CCA AAA CCT GTG GAG ATG GTG GAA	834
	Val Thr Glu Asn Il Trp Lys Ala Pro Lys Pro Val Glu Met Val Glu	
	235 240 245	
5	AAC TCA ACT GAT CCT CAC CCC ATC AAA ATC ACT CAG GTG CGG TGG AAT	882
	Asn Ser Thr Asp Pro His Pro Ile Lys Ile Thr Gln Val Arg Trp Asn	
	250 255 260 265	
	GAT CCC GGT GCA CAA TAT TCC TTA GTT GAC AAA GAG AAG CTG CCA AGA	930
	Asp Pro Gly Ala Gln Tyr Ser Leu Val Asp Lys Glu Lys Leu Pro Arg	
	270 275 280	
10	TTC CCA TTT TCA ATT GAC CAG GAA GGA GAT ATT TAC GTG ACT CAG CCC	978
	Phe Pro Phe Ser Ile Asp Gln Glu Gly Asp Ile Tyr Val Thr Gln Pro	
	285 290 295	
	TTG GAC CGA GAA GAA AAG GAT GCA TAT GTT TTT TAT GCA GTT GCA AAG	1026
	Leu Asp Arg Glu Glu Lys Asp Ala Tyr Val Phe Tyr Ala Val Ala Lys	
	300 305 310	
15	GAT GAG TAC GGA AAA CCA CTT TCA TAT CCG CTG GAA ATT CAT GTA AAA	1074
	Asp Glu Tyr Gly Lys Pro Leu Ser Tyr Pro Leu Glu Ile His Val Lys	
	315 320 325	
	GTT AAA GAT ATT AAT GAT AAT CCA CCT ACA TGT CCG TCA CCA GTA ACC	1122
	Val Lys Asp Ile Asn Asp Asn Pro Pro Thr Cys Pro Ser Pro Val Thr	
	330 335 340 345	
	GTA TTT GAG GTC CAG GAG AAT GAA CGA CTG GGT AAC AGT ATC GGG ACC	1170
	Val Phe Glu Val Gln Glu Asn Glu Arg Leu Gly Asn Ser Ile Gly Thr	
	350 355 360	
20	CTT ACT GCA CAT GAC AGG GAT GAA GAA AAT ACT GCC AAC AGT TTT CTA	1218
	Leu Thr Ala His Asp Arg Asp Glu Glu Asn Thr Ala Asn Ser Phe Leu	
	365 370 375	
	AAC TAC AGG ATT GTG GAG CAA ACT CCC AAA CTT CCC ATG GAT GGA CTC	1266
	Asn Tyr Arg Ile Val Glu Gln Thr Pro Lys Leu Pro Met Asp Gly Leu	
	380 385 390	
25	TTC CTA ATC CAA ACC TAT GCT GGA ATG TTA CAG TTA GCT AAA CAG TCC	1314
	Phe Leu Ile Gln Thr Tyr Ala Gly Met Leu Gln Leu Ala Lys Gln Ser	
	395 400 405	
	TTG AAG AAG CAA GAT ACT CCT CAG TAC AAC TTA ACG ATA GAG GTG TCT	1362
	Leu Lys Lys Gln Asp Thr Pro Gln Tyr Asn Leu Thr Ile Glu Val Ser	
	410 415 420 425	
30	GAC AAA GAT TTC AAG ACC CTT TGT TTT GTG CAA ATC AAC GTT ATT GAT	1410
	Asp Lys Asp Phe Lys Thr Leu Cys Phe Val Gln Ile Asn Val Ile Asp	
	430 435 440	
	ATC AAT GAT CAG ATC CCC ATC TTT GAA AAA TCA GAT TAT GGA AAC CTG	1458
	Ile Asn Asp Gln Ile Pro Ile Phe Glu Lys Ser Asp Tyr Gly Asn Leu	
	445 450 455	
35	ACT CTT GCT GAA GAC ACA AAC ATT GGG TCC ACC ATC TTA ACC ATC CAG	1506
	Thr Leu Ala Glu Asp Thr Asn Ile Gly Ser Thr Ile Leu Thr Ile Gln	
	460 465 470	
	GCC ACT GAT GCT GAT GAG CCA TTT ACT GGG AGT TCT AAA ATT CTG TAT	1554
	Ala Thr Asp Ala A p Glu Pro Phe Thr Gly Ser Ser Lys Ile Leu Tyr	

	475	480	485	
	CAT ATC ATA AAG GGA GAC AGT GAG GGA CGC CTG GGG GTT GAC ACA GAT			1602
	His Ile Ile Lys Gly Asp S r Glu Gly Arg Leu Gly Val Asp Thr Asp			
	490	495	500	505
5	CCC CAT ACC AAC ACC GGA TAT GTC ATA ATT AAA AAG CCT CTT GAT TTT			1650
	Pro His Thr Asn Thr Gly Tyr Val Ile Ile Lys Lys Pro Leu Asp Phe			
		510	515	520
	GAA ACA GCA GCT GTT TCC AAC ATT GTG TTC AAA GCA GAA AAT CCT GAG			1698
	Glu Thr Ala Ala Val Ser Asn Ile Val Phe Lys Ala Glu Asn Pro Glu			
		525	530	535
10	CCT CTA GTG TTT GGT GTG AAG TAC AAT GCA AGT TCT TTT GCC AAG TTC			1746
	Pro Leu Val Phe Gly Val Lys Tyr Asn Ala Ser Ser Phe Ala Lys Phe			
		540	545	550
	ACG CTT ATT GTG ACA GAT GTG AAT GAA GCA CCT CAA TTT TCC CAA CAC			1794
	Thr Leu Ile Val Thr Asp Val Asn Glu Ala Pro Gln Phe Ser Gln His			
		555	560	565
	GTA TTC CAA GCG AAA GTC AGT GAG GAT GTA GCT ATA GGC ACT AAA GTG			1842
	Val Phe Gln Ala Lys Val Ser Glu Asp Val Ala Ile Gly Thr Lys Val			
		570	575	580
15	GGC AAT GTG ACT GCC AAG GAT CCA GAA GGT CTG GAC ATA AGC TAT TCA			1890
	Gly Asn Val Thr Ala Lys Asp Pro Glu Gly Leu Asp Ile Ser Tyr Ser			
		590	595	600
	CTG AGG GGA GAC ACA AGA GGT TGG CTT AAA ATT GAC CAC GTG ACT GGT			1938
	Leu Arg Gly Asp Thr Arg Gly Trp Leu Lys Ile Asp His Val Thr Gly			
		605	610	615
20	GAG ATC TTT AGT GTG GCT CCA TTG GAC AGA GAA GCC GGA AGT CCA TAT			1986
	Glu Ile Phe Ser Val Ala Pro Leu Asp Arg Glu Ala Gly Ser Pro Tyr			
		620	625	630
	CGG GTA CAA GTG GTG GCC ACA GAA GTA GGG GGG TCT TCC TTA AGC TCT			2034
	Arg Val Gln Val Val Ala Thr Glu Val Gly Gly Ser Ser Leu Ser Ser			
		635	640	645
25	GTG TCA GAG TTC CAC CTG ATC CTT ATG GAT GTG AAT GAC AAC CCT CCC			2082
	Val Ser Glu Phe His Leu Ile Leu Met Asp Val Asn Asp Asn Pro Pro			
		650	655	660
	AGG CTA GCC AAG GAC TAC ACG GGC TTG TTC TTC TGC CAT CCC CTC AGT			2130
	Arg Leu Ala Lys Asp Tyr Thr Gly Leu Phe Phe Cys His Pro Leu Ser			
		670	675	680
30	GCA CCT GGA AGT CTC ATT TTC GAG GCT ACT GAT GAT GAT CAG CAC TTA			2178
	Ala Pro Gly Ser Leu Ile Phe Glu Ala Thr Asp Asp Asp Gln His Leu			
		685	690	695
	TTT CGG GGT CCC CAT TTT ACA TTT TCC CTC GGC AGT GGA AGC TTA CAA			2226
	Phe Arg Gly Pro His Phe Thr Phe Ser Leu Gly Ser Gly Ser Leu Gln			
		700	705	710
	AAC GAC TGG GAA GTT TCC AAA ATC AAT GGT ACT CAT GCC CGA CTG TCT			2274
	Asn Asp Trp Glu Val Ser Lys Ile Asn Gly Thr His Ala Arg Leu Ser			
		715	720	725
35	ACC AGG CAC ACA GAC TTT GAG GAG AGG GCG TAT GTC GTC TTG ATC CGC			2322
	Thr Arg His Thr Asp Phe Glu Glu Arg Ala Tyr Val Val Leu Ile Arg			
		730	735	740
				745

	ATC AAT GAT GGG GGT CGG CCA CCC TTG GAA GGC ATT GTT TCT TTA CCA	2370
	Ile Asn Asp Gly Gly Arg Pro Pro Leu Glu Gly Ile Val Ser Leu Pro	
	750 755 760	
	GTT ACA TTC TGC AGT TGT GTG GAA GGA AGT TGT TTC CGG CCA GCA GGT	2418
	Val Thr Phe Cys Ser Cys Val Glu Gly Ser Cys Phe Arg Pro Ala Gly	
	765 770 775	
5	CAC CAG ACT GGG ATA CCC ACT GTG GGC ATG GCA GTT GGT ATA CTG CTG	2466
	His Gln Thr Gly Ile Pro Thr Val Gly Met Ala Val Gly Ile Leu Leu	
	780 785 790	
	ACC ACC CTT CTG GTG ATT GGT ATA ATT TTA GCA GTT GTG TTT ATC CGC	2514
	Thr Thr Leu Leu Val Ile Ile Ile Leu Ala Val Val Phe Ile Arg	
	795 800 805	
10	ATA AAG AAG GAT AAA GGC AAA GAT AAT GTT GAA AGT GCT CAA GCA TCT	2562
	Ile Lys Lys Asp Lys Gly Lys Asp Asn Val Glu Ser Ala Gln Ala Ser	
	810 815 820 825	
	GAA GTC AAA CCT CTG AGA AGC TGAATTTGAA AAGGAATGTT TGAATTTATA TAGC	2617
	Glu Val Lys Pro Leu Arg Ser	
	830	
	AAGTGCTATT TCAGCAACAA CCATCTCATC CTATTACTTT TCATCTAACG TGCATTATAA	2677
15	TTTTTTAAAC AGATATTCCC TCTGTGCCTT TAATATTTGC TAAATATTTT TTTTTGAGG	2737
	TGGAGTCTTG CTCTGTGCCC CAGGCTGGAG TACAGTGGTG TGATCCCAGC TCACTGCAAC	2797
	CTCGCCTCC TGGGTTTACA TGATTCTCCT GCCTCAGCTT CCTAAGTAGC TGGGTTTACA	2857
	GGCACCCACC ACCATGCCCA GCTAATTTTT GTATTTTAA TAGAGACGGG GTTTCGCCAT	2917
	TTGGCCAGGC TGGTCTTGAA CTCCTGACGT CAAGTGATCT GCCTGCCTTG GTCTCCCAAT	2977
	ACAGGCATGA ACCACTGCAC CCACCTACTT AGATATTCA TGTGCTATAG ACATTAGAGA	3037
	GATTTTTTCAT TTTTCCATGA CATTITTCCT CTCTGCAAAT GGCTTAGCTA CTTGTGTTTT	3097
	TCCCTTTTGG GGCAAGACAG ACTCATTAAA TATTCTGTAC ATTTTTTCTT TATCAAGGAG	3157
	ATATATCAGT GTTGCTCAT AGAAGTGCCT GGATTCCATT TATGTTTTTT CTGATTCCAT	3217
20	CCTGTGTCCC CTTCATCCTT GACTCCTTG GTATTTCACT GAATTTCAAA CATTGTGTCAG	3277
	AGAAGAAAAA AGTGAGGACT CAGGAAAAAT AAATAAATAA AAGAACAGCC TTTTGCGGCC	3337
	GCGAATTC	3345

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

	Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr	
	1 5 10 15	
30	Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys	
	20 25 30	
	Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile	
	35 40 45	
	Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly	
	50 55 60	
	Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr	
	65 70 75 80	
	Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val	
	85 90 95	
35	Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile	
	100 105 110	
	Thr Il Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln	
	115 120 125	

Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro  
 130 135 140  
 Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn  
 145 150 155 160  
 Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn  
 165 170 175  
 Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr  
 180 185 190  
 5 Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn  
 195 200 205  
 Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe  
 210 215 220  
 Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys  
 225 230 235 240  
 Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro  
 245 250 255  
 10 Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser  
 260 265 270  
 Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln  
 275 280 285  
 Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp  
 290 295 300  
 Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu  
 305 310 315 320  
 Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn  
 325 330 335  
 15 Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn  
 340 345 350  
 Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp  
 355 360 365  
 Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln  
 370 375 380  
 Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala  
 385 390 395 400  
 20 Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro  
 405 410 415  
 Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu  
 420 425 430  
 Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile  
 435 440 445  
 Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn  
 450 455 460  
 Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro  
 465 470 475 480  
 25 Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser  
 485 490 495  
 Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr  
 500 505 510  
 Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn  
 515 520 525  
 Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys  
 530 535 540  
 30 Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val  
 545 550 555 560  
 Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser  
 565 570 575  
 Glu Asp Val Ala Ile Gly Thr Lys Val Gly Asn Val Thr Ala Lys Asp  
 580 585 590  
 Pro Glu Gly Leu Asp Ile Ser Tyr Ser Leu Arg Gly Asp Thr Arg Gly  
 595 600 605  
 Trp Leu Lys Ile Asp His Val Thr Gly Glu Ile Phe Ser Val Ala Pro  
 610 615 620  
 35 Leu Asp Arg Glu Ala Gly Ser Pro Tyr Arg Val Gln Val Val Ala Thr  
 625 630 635 640  
 Glu Val Gly Gly Ser S r Leu Ser Ser Val Ser Glu Phe His Leu Ile  
 645 650 655

Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr  
 660 665 670  
 Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser L u Ile Phe  
 675 680 685  
 Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr  
 690 695 700  
 Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys  
 705 710 715 720  
 5 Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Asp Phe Glu  
 725 730 735  
 Glu Arg Ala Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro  
 740 745 750  
 Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val  
 755 760 765  
 Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr  
 770 775 780  
 10 Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly  
 785 790 795 800  
 Ile Ile Leu Ala Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys  
 805 810 815  
 Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser  
 820 825 830

(2) INFORMATION FOR SEQ ID NO:179:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1827 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

20 Met Ala Arg Lys Lys Phe Ser Gly Leu Glu Ile Ser Leu Ile Val Leu  
 1 5 10 15  
 Phe Val Ile Val Thr Ile Ile Ala Ile Ala Leu Ile Val Val Leu Ala  
 20 25 30  
 Thr Lys Thr Pro Ala Val Asp Glu Ile Ser Asp Ser Thr Ser Thr Pro  
 35 40 45  
 Ala Thr Thr Arg Val Thr Thr Asn Pro Ser Asp Ser Gly Lys Cys Pro  
 50 55 60  
 25 Asn Val Leu Asn Asp Pro Val Asn Val Arg Ile Asn Cys Ile Pro Glu  
 65 70 75 80  
 Gln Phe Pro Thr Glu Gly Ile Cys Ala Gln Arg Gly Cys Cys Trp Arg  
 85 90 95  
 Pro Trp Asn Asp Ser Leu Ile Pro Trp Cys Phe Phe Val Asp Asn His  
 100 105 110  
 Gly Tyr Asn Val Gln Asp Met Thr Thr Thr Ser Ile Gly Val Glu Ala  
 115 120 125  
 Lys Leu Asn Arg Ile Pro Ser Pro Thr Leu Phe Gly Asn Asp Ile Asn  
 130 135 140  
 30 Ser Val Leu Phe Thr Thr Gln Asn Gln Thr Pro Asn Arg Phe Arg Phe  
 145 150 155 160  
 Lys Ile Thr Asp Pro Asn Asn Arg Arg Tyr Glu Val Pro His Gln Tyr  
 165 170 175  
 Val Lys Glu Phe Thr Gly Pro Thr Val Ser Asp Thr Leu Tyr Asp Val  
 180 185 190  
 Lys Val Ala Gln Asn Pro Phe Ser Ile Gln Val Ile Arg Lys Ser Asn  
 195 200 205  
 35 Gly Lys Thr Leu Phe Asp Thr Ser Ile Gly Pro Leu Val Tyr Ser Asp  
 210 215 220  
 Gln Tyr Leu Gln Ile Ser Ala Arg Leu Pro Ser Asp Tyr Ile Tyr Gly  
 225 230 235 240  
 Ile Gly Glu Gln Val His Lys Arg Phe Arg His Asp Leu Ser Trp Lys

100-10000-01300000

Thr Trp Pro Il 245 Phe Thr Arg Asp Gln Leu Pro Gly Asp Asn Asn Asn 255  
260 265 270  
Asn Leu Tyr Gly His Gln Thr Phe Phe Met Cys Ile Glu Asp Thr Ser 285  
275 280  
Gly Lys Ser Phe Gly Val Phe Leu Met Asn Ser Asn Ala Met Glu Ile 300  
290 295  
5 Phe Ile Gln Pro Thr Pro Ile Val Thr Tyr Arg Val Thr Gly Gly Ile 320  
305 310 315  
Leu Asp Phe Tyr Ile Leu Leu Gly Asp Thr Pro Glu Gln Val Val Gln 335  
325 330  
Gln Tyr Gln Gln Leu Val Gly Leu Pro Ala Met Pro Ala Tyr Trp Asn 350  
340 345  
Leu Gly Phe Gln Leu Ser Arg Trp Asn Tyr Lys Ser Leu Asp Val Val 365  
355 360  
10 Lys Glu Val Val Arg Arg Asn Arg Glu Ala Gly Ile Pro Phe Asp Thr 380  
370 375  
Gln Val Thr Asp Ile Asp Tyr Met Glu Asp Lys Lys Asp Phe Thr Tyr 400  
385 390 395  
Asp Gln Val Ala Phe Asn Gly Leu Pro Gln Phe Val Gln Asp Leu His 415  
405 410 415  
Asp His Gly Gln Lys Tyr Val Ile Ile Leu Asp Pro Ala Ile Ser Ile 430  
420 425 430  
Gly Arg Arg Ala Asn Gly Thr Thr Tyr Ala Thr Tyr Glu Arg Gly Asn 445  
435 440 445  
15 Thr Gln His Val Trp Ile Asn Glu Ser Asp Gly Ser Thr Pro Ile Ile 460  
450 455 460  
Gly Glu Val Trp Pro Gly Leu Thr Val Tyr Pro Asp Phe Thr Asn Pro 480  
465 470 475  
Asn Cys Ile Asp Trp Trp Ala Asn Glu Cys Ser Ile Phe His Gln Glu 495  
485 490 495  
Val Gln Tyr Asp Gly Leu Trp Ile Asp Met Asn Glu Val Ser Ser Phe 510  
500 505 510  
Ile Gln Gly Ser Thr Lys Gly Cys Asn Val Asn Lys Leu Asn Tyr Pro 525  
515 520 525  
20 Pro Phe Thr Pro Asp Ile Leu Asp Lys Leu Met Tyr Ser Lys Thr Ile 540  
530 535 540  
Cys Met Asp Ala Val Gln Asn Trp Gly Lys Gln Tyr Asp Val His Ser 560  
545 550 555  
Leu Tyr Gly Tyr Ser Met Ala Ile Ala Thr Glu Gln Ala Val Gln Lys 575  
565 570 575  
Val Phe Pro Asn Lys Arg Ser Phe Ile Leu Thr Arg Ser Thr Phe Ala 590  
580 585 590  
25 Gly Ser Gly Arg His Ala Ala His Trp Leu Gly Asp Asn Thr Ala Ser 605  
595 600 605  
Trp Glu Gln Met Glu Trp Ser Ile Thr Gly Met Leu Glu Phe Ser Leu 620  
610 615 620  
Phe Gly Ile Pro Leu Val Gly Ala Asp Ile Cys Gly Phe Val Ala Glu 640  
625 630 635  
Thr Thr Glu Glu Leu Cys Arg Arg Trp Met Gln Leu Gly Ala Phe Tyr 655  
645 650 655  
Pro Phe Ser Arg Asn His Asn Ser Asp Gly Tyr Glu His Gln Asp Pro 670  
660 665 670  
30 Ala Phe Phe Gly Gln Asn Ser Leu Leu Val Lys Ser Ser Arg Gln Tyr 685  
675 680 685  
Leu Thr Ile Arg Tyr Thr Leu Leu Pro Phe Leu Tyr Thr Leu Phe Tyr 700  
690 695 700  
Lys Ala His Val Phe Gly Glu Thr Val Ala Arg Pro Val Leu His Glu 720  
705 710 715  
Phe Tyr Glu Asp Thr Asn Ser Trp Ile Glu Asp Thr Glu Phe Leu Trp 735  
725 730 735  
35 Gly Pro Ala Leu Leu Ile Thr Pro Val Leu Lys Gln Gly Ala Asp Thr 750  
740 745 750  
Val Ser Ala Tyr Ile Pro Asp Ala Ile Trp Tyr Asp Tyr Glu Ser Gly 765  
755 760 765  
Ala Lys Arg Pro Trp Arg Lys Gln Arg Val Asp Met Tyr Leu Pro Ala

770 775 780  
 Asp Lys Ile Gly L u His Leu Arg Gly Gly Tyr Il Ile Pro Il Gln  
 785 790 795 800  
 Glu Pro Asp Val Thr Thr Thr Ala Ser Arg Lys Asn Pro Leu Gly Leu  
 805 810 815  
 Ile Val Ala Leu Gly Glu Asn Asn Thr Ala Lys Gly Asp Phe Phe Trp  
 820 825 830  
 5 Asp Asp Gly Glu Thr Lys Asp Thr Ile Gln Asn Gly Asn Tyr Ile Leu  
 835 840 845  
 Tyr Thr Phe Ser Val Ser Asn Asn Thr Leu Asp Ile Val Cys Thr His  
 850 855 860  
 Ser Ser Tyr Gln Glu Gly Thr Thr Leu Ala Phe Gln Thr Val Lys Ile  
 865 870 875 880  
 Leu Gly Leu Thr Asp Ser Val Thr Glu Val Arg Val Ala Glu Asn Asn  
 885 890 895  
 Gln Pro Met Asn Ala His Ser Asn Phe Thr Tyr Asp Ala Ser Asn Gln  
 900 905 910  
 10 Val Leu Leu Ile Ala Asp Leu Lys Leu Asn Leu Gly Arg Asn Phe Ser  
 915 920 925  
 Val Gln Trp Asn Gln Ile Phe Ser Glu Asn Glu Arg Phe Asn Cys Tyr  
 930 935 940  
 Pro Asp Ala Asp Leu Ala Thr Glu Gln Lys Cys Thr Gln Arg Gly Cys  
 945 950 955 960  
 Val Trp Arg Thr Gly Ser Ser Leu Ser Lys Ala Pro Glu Cys Tyr Phe  
 965 970 975  
 15 Pro Arg Gln Asp Asn Ser Tyr Ser Val Asn Ser Ala Arg Tyr Ser Ser  
 980 985 990  
 Met Gly Ile Thr Ala Asp Leu Gln Leu Asn Thr Ala Asn Ala Arg Ile  
 995 1000 1005  
 Lys Leu Pro Ser Asp Pro Ile Ser Thr Leu Arg Val Glu Val Lys Tyr  
 1010 1015 1020  
 His Lys Asn Asp Met Leu Gln Phe Lys Ile Tyr Asp Pro Gln Lys Lys  
 1025 1030 1035 1040  
 Arg Tyr Glu Val Pro Val Pro Leu Asn Ile Pro Thr Thr Pro Ile Ser  
 1045 1050 1055  
 20 Thr Tyr Glu Asp Arg Leu Tyr Asp Val Glu Ile Lys Glu Asn Pro Phe  
 1060 1065 1070  
 Gly Ile Gln Ile Arg Arg Arg Ser Ser Gly Arg Val Ile Trp Asp Ser  
 1075 1080 1085  
 Trp Leu Pro Gly Phe Ala Phe Asn Asp Gln Phe Ile Gln Ile Ser Thr  
 1090 1095 1100  
 Arg Leu Pro Ser Glu Tyr Ile Tyr Gly Phe Gly Glu Val Glu His Thr  
 1105 1110 1115 1120  
 25 Ala Phe Lys Arg Asp Leu Asn Trp Asn Thr Trp Gly Met Phe Thr Arg  
 1125 1130 1135  
 Asp Gln Pro Pro Gly Tyr Lys Leu Asn Ser Tyr Gly Phe His Pro Tyr  
 1140 1145 1150  
 Tyr Met Ala Leu Glu Glu Glu Gly Asn Ala His Gly Val Phe Leu Leu  
 1155 1160 1165  
 Asn Ser Asn Ala Met Asp Val Thr Phe Gln Pro Thr Pro Ala Leu Thr  
 1170 1175 1180  
 Tyr Arg Thr Val Gly Gly Ile Leu Asp Phe Tyr Met Phe Leu Gly Pro  
 1185 1190 1195 1200  
 30 Thr Pro Gln Val Ala Thr Lys Gln Tyr His Glu Val Ile Gly His Pro  
 1205 1210 1215  
 Val Met Pro Ala Tyr Trp Ala Leu Gly Phe Gln Leu Cys Arg Tyr Gly  
 1220 1225 1230  
 Tyr Ala Asn Thr Ser Glu Val Arg Glu Leu Tyr Asp Ala Met Val Ala  
 1235 1240 1245  
 Ala Asn Ile Pro Tyr Asp Val Gln Tyr Thr Asp Ile Asp Tyr Met Glu  
 1250 1255 1260  
 35 Arg Gln Leu Asp Phe Thr Ile Gly Glu Ala Phe Gln Asp Leu Pro Gln  
 1265 1270 1275 1280  
 Phe Val Asp Lys Ile Arg Gly Glu Gly Met Arg Tyr Ile Ile Ile Leu  
 1285 1290 1295  
 Asp Pro Ala Ile Ser Gly Asn Glu Thr Lys Thr Tyr Pro Ala Ph Glu

1300 1305 1310  
 Arg Gly Gln Gln Asn Asp Val Phe Val Lys Trp Pro Asn Thr Asn Asp  
 1315 1320 1325  
 Ile Cys Trp Ala Lys Val Trp Pro Asp Leu Pro Asn Ile Thr Ile Asp  
 1330 1335 1340  
 Lys Thr Leu Thr Glu Asp Glu Ala Val Asn Ala Ser Arg Ala His Val  
 345 1350 1355 1360  
 5 Ala Phe Pro Asp Phe Phe Arg Thr Ser Thr Ala Glu Trp Trp Ala Arg  
 1365 1370 1375  
 Glu Ile Val Asp Phe Tyr Asn Glu Lys Met Lys Phe Asp Gly Leu Trp  
 1380 1385 1390  
 Ile Asp Met Asn Glu Pro Ser Ser Phe Val Asn Gly Thr Thr Thr Asn  
 1395 1400 1405  
 Gln Cys Arg Asn Asp Glu Leu Asn Tyr Pro Pro Tyr Phe Pro Glu Leu  
 1410 1415 1420  
 Thr Lys Arg Thr Asp Gly Leu His Phe Arg Thr Ile Cys Met Glu Ala  
 425 1430 1435 1440  
 10 Glu Gln Ile Leu Ser Asp Gly Thr Ser Val Leu His Tyr Asp Val His  
 1445 1450 1455  
 Asn Leu Tyr Gly Trp Ser Gln Met Lys Pro Thr His Asp Ala Leu Gln  
 1460 1465 1470  
 Lys Thr Thr Gly Lys Arg Gly Ile Val Ile Ser Arg Ser Thr Tyr Pro  
 1475 1480 1485  
 Thr Ser Gly Arg Trp Gly Gly His Trp Leu Gly Asp Asn Tyr Ala Arg  
 1490 1495 1500  
 15 Trp Asp Asn Met Asp Lys Ser Ile Ile Gly Met Met Glu Phe Ser Leu  
 505 1510 1515 1520  
 Phe Gly Ile Ser Tyr Thr Gly Ala Asp Ile Cys Gly Phe Phe Asn Asn  
 1525 1530 1535  
 Ser Glu Tyr His Leu Cys Thr Arg Trp Met Gln Leu Gly Ala Phe Tyr  
 1540 1545 1550  
 Pro Tyr Ser Arg Asn His Asn Ile Ala Asn Thr Arg Arg Gln Asp Pro  
 1555 1560 1565  
 Ala Ser Trp Asn Glu Thr Phe Ala Glu Met Ser Arg Asn Ile Leu Asn  
 1570 1575 1580  
 20 Ile Arg Tyr Thr Leu Leu Pro Tyr Phe Tyr Thr Gln Met His Glu Ile  
 585 1590 1595 1600  
 His Ala Asn Gly Gly Thr Val Ile Arg Pro Leu Leu His Glu Phe Phe  
 1605 1610 1615  
 Asp Glu Lys Pro Thr Trp Asp Ile Phe Lys Gln Phe Leu Trp Gly Pro  
 1620 1625 1630  
 Ala Phe Met Val Thr Pro Val Leu Glu Pro Tyr Val Gln Thr Val Asn  
 1635 1640 1645  
 25 Ala Tyr Val Pro Asn Ala Arg Trp Phe Asp Tyr His Thr Gly Lys Asp  
 1650 1655 1660  
 Ile Gly Val Arg Gly Gln Phe Gln Thr Phe Asn Ala Ser Tyr Asp Thr  
 665 1670 1675 1680  
 Ile Asn Leu His Val Arg Gly Gly His Ile Leu Pro Cys Gln Glu Pro  
 1685 1690 1695  
 Ala Gln Asn Thr Phe Tyr Ser Arg Gln Lys His Met Lys Leu Ile Val  
 1700 1705 1710  
 Ala Ala Asp Asp Asn Gln Met Ala Gln Gly Ser Leu Phe Trp Asp Asp  
 1715 1720 1725  
 30 Gly Glu Ser Ile Asp Thr Tyr Glu Arg Asp Leu Tyr Leu Ser Val Gln  
 1730 1735 1740  
 Phe Asn Leu Asn Gln Thr Thr Leu Thr Ser Thr Ile Leu Lys Arg Gly  
 745 1750 1755 1760  
 Tyr Ile Asn Lys Ser Glu Thr Arg Leu Gly Ser Leu His Val Trp Gly  
 1765 1770 1775  
 Lys Gly Thr Thr Pro Val Asn Ala Val Thr Leu Thr Tyr Asn Gly Asn  
 1780 1785 1790  
 35 Lys Asn Ser Leu Pro Phe Asn Glu Asp Thr Thr Asn Met Ile Leu Arg  
 1795 1800 1805  
 Ile Asp Leu Thr Thr His Asn Val Thr Leu Glu Glu Pro Ile Glu Ile  
 1810 1815 1820  
 Asn Trp Ser



## (2) INFORMATION FOR SEQ ID NO:180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 45...2099  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GCCTTACTGC AGGAAGGCAC TCCGAAGACA TAAGTCGGTG AGAC ATG GCT GAA GAT 56  
 Met Ala Glu Asp  
 1

AAA AGC AAG AGA GAC TCC ATC GAG ATG AGT ATG AAG GGA TGC CAG ACA 104  
 Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys Gly Cys Gln Thr  
 5 10 15 20

AAC AAC GGG TTT GTC CAT AAT GAA GAC ATT CTG GAG CAG ACC CCG GAT 152  
 Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu Gln Thr Pro Asp  
 25 30 35

CCA GGC AGC TCA ACA GAC AAC CTG AAG CAC AGC ACC AGG GGC ATC CTT 200  
 Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr Arg Gly Ile Leu  
 40 45 50

GGC TCC CAG GAG CCC GAC TTC AAG GGC GTC CAG CCC TAT GCG GGG ATG 248  
 Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro Tyr Ala Gly Met  
 55 60 65

CCC AAG GAG GTG CTG TTC CAG TTC TCT GGC CAG GCC CGC TAC CGC ATA 296  
 Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala Arg Tyr Arg Ile  
 70 75 80

CCT CGG GAG ATC CTC TTC TGG CTC ACA GTG GCT TCT GTG CTG GTG CTC 344  
 Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser Val Leu Val Leu  
 85 90 95 100

ATC GCG GCC ACC ATA GCC ATC ATT GCC CTC TCT CCA AAG TGC CTA GAC 392  
 Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro Lys Cys Leu Asp  
 105 110 115

TGG TGG CAG GAG GGG CCC ATG TAC CAG ATC TAC CCA AGG TCT TTC AAG 440  
 Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro Arg Ser Phe Lys  
 120 125 130

GAC AGT AAC AAG GAT GGG AAC GGA GAT CTG AAA GGT ATT CAA GAT AAA 488  
 Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly Ile Gln Asp Lys  
 135 140 145

CTG GAC TAC ATC ACA GCT TTA AAT ATA AAA ACT GTT TGG ATT ACT TCA 536  
 Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val Trp Ile Thr Ser  
 150 155 160

TTT TAT AAA TCG TCC CTT AAA GAT TTC AGA TAT GGT GTT GAA GAT TTC 584  
 Ph Tyr Lys Ser Ser L u Lys Asp Phe Arg Tyr Gly Val Glu Asp Phe

	165	170	175	180	
	CGG GAA GTT GAT CCC ATT TTT GGA ACG ATG GAA GAT TTT GAG AAT CTG				632
	Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp Phe Glu Asn Leu				
		185	190	195	
5	GTT GCA GCC ATA CAT GAT AAA GGT TTA AAA TTA ATC ATC GAT TTC ATA				680
	Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile Ile Asp Phe Ile				
		200	205	210	
	CCA AAC CAC ACG AGT GAT AAA CAT ATT TGG TTT CAA TTG AGT CGG ACA				728
	Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln Leu Ser Arg Thr				
		215	220	225	
10	CGG ACA GGA AAA TAT ACT GAT TAT TAT ATC TGG CAT GAC TGT ACC CAT				776
	Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His Asp Cys Thr His				
		230	235	240	
	GAA AAT GGC AAA ACC ATT CCA CCC AAC AAC TGG TTA AGT GTG TAT GGA				824
	Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu Ser Val Tyr Gly				
		245	250	255	260
	AAC TCC AGT TGG CAC TTT GAC GAA GTG CGA AAC CAA TGT TAT TTT CAT				872
	Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln Cys Tyr Phe His				
		265	270	275	
15	CAG TTT ATG AAA GAG CAA CCT GAT TTA AAT TTC CGC AAT CCT GAT GTT				920
	Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg Asn Pro Asp Val				
		280	285	290	
	CAA GAA GAA ATA AAA GAA ATT TTA CGG TTC TGG CTC ACA AAG GGT GTT				968
	Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu Thr Lys Gly Val				
		295	300	305	
20	GAT GGT TTT AGT TTG GAT GCT GTT AAA TTC CTC CTA GAA GCA AAG CAC				1016
	Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu Glu Ala Lys His				
		310	315	320	
	CTG AGA GAT GAG ATC CAA GTA AAT AAG ACC CAA ATC CCG GAC ACG GTC				1064
	Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile Pro Asp Thr Val				
		325	330	335	340
25	ACA CAA TAC TCG GAG CTG TAC CAT GAC TTC ACC ACC ACG CAG GTG GGA				1112
	Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr Thr Gln Val Gly				
		345	350	355	
	ATG CAC GAC ATT GTC CGC AGC TTC CGG CAG ACC ATG GAC CAA TAC AGC				1160
	Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met Asp Gln Tyr Ser				
		360	365	370	
30	ACG GAG CCC GGC AGA TAC AGG TTC ATG GGG ACT GAA GCC TAT GCA GAG				1208
	Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu Ala Tyr Ala Glu				
		375	380	385	
	AGT ATT GAC AGG ACC GTG ATG TAC TAT GGA TTG CCA TTT ATC CAA GAA				1256
	Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro Phe Ile Gln Glu				
		390	395	400	
	GCT GAT TTT CCC TTC AAC AAT TAC CTC AGC ATG CTA GAC ACT GTT TCT				1304
	Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu Asp Thr Val Ser				
		405	410	415	420
35	GGG AAC AGC GTG TAT GAG GTT ATC ACA TCC TGG ATG GAA AAC ATG CCA				1352
	Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp Met Glu Asn Met Pro				
		425	430	435	

GAA GGA AAA TGG CCT AAC TGG ATG ATT GGT GGA CCA GAC AGT TCA CGG 1400  
 Glu Gly Lys Trp Pro Asn Trp Met Il Gly Gly Pro Asp Ser Ser Arg  
 440 445 450

CTG ACT TCG CGT TTG GGG AAT CAG TAT GTC AAC GTG ATG AAC ATG CTT 1448  
 Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val Met Asn Met Leu  
 455 460 465

5 CTT TTC ACA CTC CCT GGA ACT CCT ATA ACT TAC TAT GGA GAA GAA ATT 1496  
 Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Gly Glu Glu Ile  
 470 475 480

GGA ATG GGA AAT ATT GTA GCC GCA AAT CTC AAT GAA AGC TAT GAT ATT 1544  
 Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu Ser Tyr Asp Ile  
 485 490 495 500

10 AAT ACC CTT CGC TCA AAG TCA CCA ATG CAG TGG GAC AAT AGT TCA AAT 1592  
 Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp Asn Ser Ser Asn  
 505 510 515

GCT GGT TTT TCT GAA GCT AGT AAC ACC TGG TTA CCT ACC AAT TCA GAT 1640  
 Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro Thr Asn Ser Asp  
 520 525 530

15 TAC CAC ACT GTG AAT GTT GAT GTC CAA AAG ACT CAG CCC AGA TCG GCT 1688  
 Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln Pro Arg Ser Ala  
 535 540 545

TTG AAG TTA TAT CAA GAT TTA AGT CTA CTT CAT GCC AAT GAG CTA CTC 1736  
 Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala Asn Glu Leu Leu  
 550 555 560

20 CTC AAC AGG GGC TGG TTT TGC CAT TTG AGG AAT GAC AGC CAC TAT GTT 1784  
 Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp Ser His Tyr Val  
 565 570 575 580

GTG TAC ACA AGA GAG CTG GAT GGC ATC GAC AGA ATC TTT ATC GTG GTT 1832  
 Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile Phe Ile Val Val  
 585 590 595

CTG AAT TTT GGA GAA TCA ACA CTG TTA AAT CTA CAT AAT ATG ATT TCG 1880  
 Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His Asn Met Ile Ser  
 600 605 610

25 GGC CTT CCC GCT AAA ATA AGA ATA AGG TTA AGT ACC AAT TCT GCC GAC 1928  
 Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr Asn Ser Ala Asp  
 615 620 625

AAA GGC AGT AAA GTT GAT ACA AGT GGC ATT TTT CTG GAC AAG GGA GAG 1976  
 Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu Asp Lys Gly Glu  
 630 635 640

30 GGA CTC ATC TTT GAA CAC AAC ACG AAG AAT CTC CTT CAT CGC CAA ACA 2024  
 Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu His Arg Gln Thr  
 645 650 655 660

GCT TTC AGA GAT AGA TGC TTT GTT TCC AAT CGA GCA TGC TAT TCC AGT 2072  
 Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala Cys Tyr Ser Ser  
 665 670 675

35 GTA CTG AAC ATA CTG TAT ACC TCG TGT TAGGCACCTT TATGAAGAGA TGAAGAC 2126  
 Val Leu Asn Ile Leu Tyr Thr Ser Cys  
 680 685

ACTGGCATT CAGTGGGATT GTAAGCATT GTAATAGCTT CATGTACAGC ATGCTGCTTG 2186  
 GTGAACAATC ATTAATTCTT CGATATTCTT GTAGCTTGAA TGTAACCGCT TTAAGAAAGG 2246

TTCTCAAATG TTTTGAAAAA AATAAAATGT TTAAAGT

2284

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Met Ala Glu Asp Lys Ser Lys Arg Asp Ser Ile Glu Met Ser Met Lys  
1 5 10 15  
10 Gly Cys Gln Thr Asn Asn Gly Phe Val His Asn Glu Asp Ile Leu Glu  
20 25 30  
Gln Thr Pro Asp Pro Gly Ser Ser Thr Asp Asn Leu Lys His Ser Thr  
35 40 45  
Arg Gly Ile Leu Gly Ser Gln Glu Pro Asp Phe Lys Gly Val Gln Pro  
50 55 60  
Tyr Ala Gly Met Pro Lys Glu Val Leu Phe Gln Phe Ser Gly Gln Ala  
65 70 75 80  
Arg Tyr Arg Ile Pro Arg Glu Ile Leu Phe Trp Leu Thr Val Ala Ser  
85 90 95  
15 Val Leu Val Leu Ile Ala Ala Thr Ile Ala Ile Ile Ala Leu Ser Pro  
100 105 110  
Lys Cys Leu Asp Trp Trp Gln Glu Gly Pro Met Tyr Gln Ile Tyr Pro  
115 120 125  
Arg Ser Phe Lys Asp Ser Asn Lys Asp Gly Asn Gly Asp Leu Lys Gly  
130 135 140  
Ile Gln Asp Lys Leu Asp Tyr Ile Thr Ala Leu Asn Ile Lys Thr Val  
145 150 155 160  
20 Trp Ile Thr Ser Phe Tyr Lys Ser Ser Leu Lys Asp Phe Arg Tyr Gly  
165 170 175  
Val Glu Asp Phe Arg Glu Val Asp Pro Ile Phe Gly Thr Met Glu Asp  
180 185 190  
Phe Glu Asn Leu Val Ala Ala Ile His Asp Lys Gly Leu Lys Leu Ile  
195 200 205  
Ile Asp Phe Ile Pro Asn His Thr Ser Asp Lys His Ile Trp Phe Gln  
210 215 220  
25 Leu Ser Arg Thr Arg Thr Gly Lys Tyr Thr Asp Tyr Tyr Ile Trp His  
225 230 235 240  
Asp Cys Thr His Glu Asn Gly Lys Thr Ile Pro Pro Asn Asn Trp Leu  
245 250 255  
Ser Val Tyr Gly Asn Ser Ser Trp His Phe Asp Glu Val Arg Asn Gln  
260 265 270  
Cys Tyr Phe His Gln Phe Met Lys Glu Gln Pro Asp Leu Asn Phe Arg  
275 280 285  
Asn Pro Asp Val Gln Glu Glu Ile Lys Glu Ile Leu Arg Phe Trp Leu  
290 295 300  
30 Thr Lys Gly Val Asp Gly Phe Ser Leu Asp Ala Val Lys Phe Leu Leu  
305 310 315 320  
Glu Ala Lys His Leu Arg Asp Glu Ile Gln Val Asn Lys Thr Gln Ile  
325 330 335  
Pro Asp Thr Val Thr Gln Tyr Ser Glu Leu Tyr His Asp Phe Thr Thr  
340 345 350  
Thr Gln Val Gly Met His Asp Ile Val Arg Ser Phe Arg Gln Thr Met  
355 360 365  
35 Asp Gln Tyr Ser Thr Glu Pro Gly Arg Tyr Arg Phe Met Gly Thr Glu  
370 375 380  
Ala Tyr Ala Glu Ser Ile Asp Arg Thr Val Met Tyr Tyr Gly Leu Pro  
385 390 395 400  
Phe Ile Gln Glu Ala Asp Phe Pro Phe Asn Asn Tyr Leu Ser Met Leu  
405 410 415

Asp Thr Val Ser Gly Asn Ser Val Tyr Glu Val Ile Thr Ser Trp M t  
 420 425 430  
 Glu Asn Met Pro Glu Gly Lys Trp Pro Asn Trp Met Ile Gly Gly Pro  
 435 440 445  
 Asp Ser Ser Arg Leu Thr Ser Arg Leu Gly Asn Gln Tyr Val Asn Val  
 450 455 460  
 Met Asn Met Leu Leu Phe Thr Leu Pro Gly Thr Pro Ile Thr Tyr Tyr  
 465 470 475 480  
 5 Gly Glu Glu Ile Gly Met Gly Asn Ile Val Ala Ala Asn Leu Asn Glu  
 485 490 495  
 Ser Tyr Asp Ile Asn Thr Leu Arg Ser Lys Ser Pro Met Gln Trp Asp  
 500 505 510  
 Asn Ser Ser Asn Ala Gly Phe Ser Glu Ala Ser Asn Thr Trp Leu Pro  
 515 520 525  
 Thr Asn Ser Asp Tyr His Thr Val Asn Val Asp Val Gln Lys Thr Gln  
 530 535 540  
 10 Pro Arg Ser Ala Leu Lys Leu Tyr Gln Asp Leu Ser Leu Leu His Ala  
 545 550 555 560  
 Asn Glu Leu Leu Leu Asn Arg Gly Trp Phe Cys His Leu Arg Asn Asp  
 565 570 575  
 Ser His Tyr Val Val Tyr Thr Arg Glu Leu Asp Gly Ile Asp Arg Ile  
 580 585 590  
 Phe Ile Val Val Leu Asn Phe Gly Glu Ser Thr Leu Leu Asn Leu His  
 595 600 605  
 Asn Met Ile Ser Gly Leu Pro Ala Lys Ile Arg Ile Arg Leu Ser Thr  
 610 615 620  
 15 Asn Ser Ala Asp Lys Gly Ser Lys Val Asp Thr Ser Gly Ile Phe Leu  
 625 630 635 640  
 Asp Lys Gly Glu Gly Leu Ile Phe Glu His Asn Thr Lys Asn Leu Leu  
 645 650 655  
 His Arg Gln Thr Ala Phe Arg Asp Arg Cys Phe Val Ser Asn Arg Ala  
 660 665 670  
 Cys Tyr Ser Ser Val Leu Asn Ile Leu Tyr Thr Ser Cys  
 675 680 685

20

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

25

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu Val Pro Arg Gly Ser Pro Gly Ile Pro Gly Ser Arg Val Gly Gln  
 1 5 10 15  
 Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His  
 20 25 30  
 Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg  
 35 40 45  
 30 Pro Leu Arg Gln Ala Ser  
 50

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

35

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Ser Ala Arg Asp S r Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg  
1 5 10 15  
Leu Asn Gly

5 (2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Gly Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr  
1 5 10 15  
Arg Lys Ser Ser Arg  
20

(2) INFORMATION FOR SEQ ID NO:185:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg  
1 5 10 15  
Arg His Pro

(2) INFORMATION FOR SEQ ID NO:186:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

30

Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ser Arg Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His  
1 5 10 15  
Ser Ser His Asn Arg  
20

5 (2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser  
1 5 10 15  
Arg Pro Asn

(2) INFORMATION FOR SEQ ID NO:189:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Arg Tyr Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser  
1 5 10 15  
Ser Ser Val Arg Gly Gly Cys Gly  
20

(2) INFORMATION FOR SEQ ID NO:190:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser Val Arg Gly Gly  
1 5 10 15  
Cys Gly Ala His Ser Ser Pro Pro Arg Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:191:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr  
1 5 10 15  
Met Val Ser Arg Leu  
20

5

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Glu Asn Ala Asn Thr Arg Lys Ser Ser Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:193:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Lys Lys Arg Ile Ala Gly Leu Pro Trp Tyr Arg Cys Arg Thr Val Ala  
1 5 10 15  
Phe Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr Ile Val Gln  
20 25 30  
Leu Ser Phe Thr Pro Glu Glu  
35

25

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:195:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

S r Asn Pro Arg Gly Arg Arg His Pro  
1 5

5 (2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Thr Asn Ala Lys His Ser Ser His Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- 15
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

20 Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- 25
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Arg Arg Leu Arg Thr Arg Ser Arg Pro Asn  
1 5 10

30 (2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Arg Val Gly Gln Cys Thr Asp S r Asp Val Arg Arg Pro Trp Ala Arg  
1 5 10 15

Ser Cys Ala

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Val Arg Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala  
1 5 10 15  
10 Gly Thr Arg Asn Ser  
20

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala  
1 5 10 15  
20 Ser Gln His

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp  
1 5 10 15  
30 Ser Asp Ser Asp Thr Met Ala Lys His Ser Ser His Asn Arg Arg Leu  
20 25 30  
Arg Thr Arg Ser Arg Pro Asn Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Tyr S r Lys Val  
1

(2) INFORMATION FOR SEQ ID NO:204:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

10 Phe Pro His Leu  
1

(2) INFORMATION FOR SEQ ID NO:205:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Tyr Arg Gly Val  
1

20 (2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Tyr Gln Thr Ile  
1

(2) INFORMATION FOR SEQ ID NO:207:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

35 Thr Glu Gln Phe  
1

(2) INFORMATION FOR SEQ ID NO:208:

5 (ii) MOLECULE TYPE: peptide  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

(2) INFORMATION FOR SEQ ID NO:209:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

(2) INFORMATION FOR SEQ ID NO:210:

20

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

(2) INFORMATION FOR SEQ ID NO:211:

30 (ii) MOLECULE TYPE: DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...714  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG 96

	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	L	u	
				20					25					30				
	TAT	GAG	CGC	GAT	GAA	GGT	GAT	AAA	TGG	CGA	AAC	AAA	AAG	TTT	GAA	TTG	144	
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	L	u	
			35				40					45						
5	GGT	TTG	GAG	TTT	CCC	AAT	CTT	CCT	TAT	TAT	ATT	GAT	GGT	GAT	GTT	AAA	192	
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
		50				55					60							
	TTA	ACA	CAG	TCT	ATG	GCC	ATC	ATA	CGT	TAT	ATA	GCT	GAC	AAG	CAC	AAC	240	
	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
		65			70			75							80			
	ATG	TTG	GGT	GGT	TGT	CCA	AAA	GAG	CGT	GCA	GAG	ATT	TCA	ATG	CTT	GAA	288	
10	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
				85					90						95			
	GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336	
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
				100				105					110					
	AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384	
15	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
			115					120					125					
	ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432	
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
			130				135					140						
	GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480	
	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
		145				150					155				160			
20	GTT	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA	528	
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
					165				170						175			
	GTT	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC	576	
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
				180				185						190				
25	TTG	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC	624	
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
			195					200					205					
	ACG	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	GTT	CCG	CGT	672	
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
		210				215						220						
30	GGA	TCC	CCA	GGA	ATT	CCC	GGG	TCG	ACT	CGA	GCG	GCC	GCA	TCG	TGA	717		
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser				
		225			230						235							

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu L u Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 5 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 10 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 15 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser  
 225 230 235

(2) INFORMATION FOR SEQ ID NO:213:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 30 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 35 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu

	Val	Cys	Phe	Lys	165	Lys	Arg	Ile	Glu	Ala	170	Ile	Pro	Gln	Ile	Asp	175	Lys	Tyr
				180	Lys	Tyr	Ile	Ala	185	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
	L	u	Lys	Ser	S	r			200					205					
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg			
	210					215						220							
5	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Ser	Gln			
	225					230					235					240			
	Gly	Ser	Lys	Gln	Cys	Met	Gln	Tyr	Arg	Thr	Gly	Arg	Leu	Thr	Val	Gly			
					245					250					255				
	Ser	Glu	Tyr	Gly	Cys	Gly	Met	Asn	Pro	Ala	Arg	His	Ala	Thr	Pro	Ala			
				260					265					270					
	Tyr	Pro	Ala	Arg	Leu	Leu	Pro	Arg	Tyr	Arg									
				275				280											

10 (2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 282 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro			
	1				5				10						15				
	Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Lys	Tyr	Glu	Glu	His	Leu					
				20				25					30						
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu			
				35				40					45						
20	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys			
	50					55					60								
	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn			
	65				70				75						80				
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu			
				85				90						95					
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser			
				100				105					110						
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu			
				115				120					125						
25	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn			
	130					135						140							
	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp			
	145					150					155				160				
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu			
				165				170						175					
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr			
				180				185						190					
30	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala			
				195				200					205						
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg			
	210					215						220							
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Ser	Asp			
	225					230					235					240			
	His	Ala	Leu	Gly	Thr	Asn	Leu	Arg	Ser	Asp	Asn	Ala	Lys	Glu	Pro	Gly			
				245				250						255					
	Asp	Tyr	Asn	Cys	Gly	Asn	Gly	Asn	Ser	Thr	Gly	Arg	Lys	Val	Phe				
			260			265							270						
35	Asn	Arg	Arg	Arg	Pro	Ser	Ala	Ile	Pro	Thr									
			275					280											

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
10 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
15 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
20 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Pro  
225 230 235 240  
Cys Gly Gly Ser Trp Gly Arg Phe Met Gln Gly Gly Leu Phe Gly Gly  
245 250 255  
Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg Thr Ser Ala Ser Leu  
260 265 270  
25 Glu Pro Pro Ser Ser Asp Tyr  
275

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
35 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn L u Pro Tyr Tyr Ile Asp Gly Asp Val Lys



50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 5 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 10 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Gly  
 225 230 235 240  
 Ser Thr Gly Thr Ala Gly Gly Glu Arg Ser Gly Val Leu Asn Leu His  
 245 250 255  
 15 Thr Arg Asp Asn Ala Ser Gly Ser Gly Phe Lys Pro Trp Tyr Pro Ser  
 260 265 270  
 Asn Arg Gly His Lys  
 275

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 277 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:217:

25 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 30 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 35 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190

Leu Lys S r Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser S r His  
 225 230 235 240  
 Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg  
 245 250 255  
 5 Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu  
 260 265 270  
 Pro Arg Gly Pro Asn  
 275

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 248 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

15 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 20 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 25 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 30 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His  
 225 230 235 240  
 Ser Gly Gly Met Asn Arg Ala Tyr  
 245

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 248 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
5 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
10 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
15 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp  
225 230 235 240  
20 Val Phe Arg Glu Leu Arg Asp Arg  
245

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

25 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
30 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
35 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn

130                      135                      140  
 Gly Asp His Val Thr His Pro Asp Ph Met Leu Tyr Asp Ala Leu Asp  
 145                      150                      155                      160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
                     165                      170                      175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Il Asp Lys Tyr  
                     180                      185                      190  
 5 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
                     195                      200                      205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
                     210                      215                      220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Trp Asn  
 225                      230                      235                      240  
 Ala Thr Ser His His Thr Arg Pro  
                     245

10 (2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1                      5                      10                      15  
 Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
                     20                      25                      30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
                     35                      40                      45  
 20 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
                     50                      55                      60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65                      70                      75                      80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
                     85                      90                      95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
                     100                      105                      110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
                     115                      120                      125  
 25 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
                     130                      135                      140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145                      150                      155                      160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
                     165                      170                      175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
                     180                      185                      190  
 30 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
                     195                      200                      205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
                     210                      215                      220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Pro  
 225                      230                      235                      240  
 Gln Leu Pro Arg Gly Pro Asn  
                     245

35 (2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 258 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

5 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1      5      10      15
Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
  20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
  35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
  50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
  65      70      75      80
10 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
   85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
  100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
  115      120      125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
  130      135      140
15 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
  145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
  165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
  180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
  195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
  210      215      220
20 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Gly Asp
  225      230      235      240
Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr
  245      250      255
Arg Pro

```

(2) INFORMATION FOR SEQ ID NO:223:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 257 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1      5      10      15
Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
  20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
  35      40      45
35 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
   50      55      60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
  65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Il Ser Met Leu Glu
  85      90      95

```

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Ph Glu Thr L u Lys Val Asp Ph L u Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 5 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 10 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Trp Asn  
 225 230 235 240  
 Ala Thr Ser His His Thr Arg Pro Thr Pro Gln Leu Pro Arg Gly Pro  
 245 250 255  
 Asn

(2) INFORMATION FOR SEQ ID NO:224:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

20 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 25 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 30 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 35 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Asp  
 225 230 235 240  
 Val Phe Arg Glu Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr

245 250 255  
Arg Pro Thr Pro Gln L u Pro Arg Gly Pro Asn  
260 265

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 277 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

10 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
15 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
20 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
25 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser His  
225 230 235 240  
Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu Leu Arg  
245 250 255  
Asp Arg Trp Asn Ala Thr Ser Ala Ala Thr Arg Pro Thr Pro Gln Leu  
260 265 270  
Pro Arg Gly Pro Asn  
275

30

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro





130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 5 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ala  
 225 230 235 240  
 Arg Asp Ser Gly Pro Ala Glu Asp Gly Ser Arg Ala Val Arg Leu Asn  
 245 250 255  
 Gly

10

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

15

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 25 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 30 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Asp Gly  
 225 230 235 240  
 Ser Arg Ala Val Arg Leu Asn Gly Val Glu Asn Ala Asn Thr Arg Lys  
 245 250 255  
 35 Ser Ser Arg

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
10 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
15 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
20 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn  
225 230 235 240  
Ala Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His  
245 250 255  
Pro

25

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
35 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn

65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Il Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Ph Leu S r Lys Leu Pro Glu  
115 120 125  
5 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
10 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Glu Asn  
225 230 235 240  
Ala Asn Thr Arg Lys Ser Ser Arg  
245

(2) INFORMATION FOR SEQ ID NO:231:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
25 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
30 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
35 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Lys  
225 230 235 240

S r S r Arg Ser Asn Pro Arg Gly  
245

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 247 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

10 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
15 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
20 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
25 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Ser Asn  
225 230 235 240  
Pro Arg Gly Arg Arg His Pro  
245

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 249 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

35 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15  
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Ph Glu Leu  
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly A p Val Lys  
 50 55 60  
 L u Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile S r Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 5 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 10 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Thr Arg  
 225 230 235 240  
 Lys Ser Ser Arg Ser Asn Pro Arg Gly  
 245  
 15

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 277 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

20

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 25 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 30 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 35 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg

210                      215                      220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Thr  
 225                      230                      235                      240  
 Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp  
                     245                      250                      255  
 Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr  
                     260                      265                      270  
 5 Arg Ser Arg Pro Asn  
                     275

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1                      5                      10                      15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20                      25                      30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35                      40                      45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50                      55                      60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65                      70                      75                      80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85                      90                      95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100                      105                      110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115                      120                      125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130                      135                      140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145                      150                      155                      160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165                      170                      175  
 25 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
                     180                      185                      190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
                     195                      200                      205  
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
                     210                      215                      220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Thr  
 225                      230                      235                      240  
 30 Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp Ser Asp  
                     245                      250                      255  
 Ser Asp

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Il Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 5 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 10 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 15 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Ser Arg  
 225 230 235 240  
 Pro Tyr Ser Val Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser  
 245 250 255  
 20 His Asn Arg

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 30 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 35 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn

130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 5 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Asn  
 225 230 235 240  
 Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg Ser Arg Pro  
 245 250 255  
 Asn

10

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

15

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 20 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 25 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 30 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Thr Asn  
 225 230 235 240  
 Ala Lys His Ser Ser His Asn  
 245

35

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1      5      10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50      55      60
10 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85      90      95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100      105      110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115      120      125
15 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130      135      140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145      150      155      160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195      200      205
20 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210      215      220
Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Ser Ser
225      230      235      240
His Asn Arg Arg Leu Arg Thr Arg
245

```

(2) INFORMATION FOR SEQ ID NO:240:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 248 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1      5      10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35      40      45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50      55      60
35 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65      70      75      80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85      90      95

```

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Ph Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Ph Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 5 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 10 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Arg  
 225 230 235 240  
 Leu Arg Thr Arg Ser Arg Pro Asn  
 245

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 282 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

20 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 25 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 30 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 35 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Val  
 225 230 235 240  
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys  
 245 250 255  
 Ala His Gln Gly Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Il

260 265 270  
 Thr Arg Pro Leu Arg Gln Ala Ser Ala His  
 275 280

(2) INFORMATION FOR SEQ ID NO:242:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

10 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 15 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 20 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 25 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Val  
 225 230 235 240  
 Gly Gln Cys Thr Asp Ser Asp Val Arg Arg Pro Trp Ala Arg Ser Cys  
 245 250 255  
 Ala

(2) INFORMATION FOR SEQ ID NO:243:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 20 25 30  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 5 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 10 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 15 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ser Val Arg  
 225 230 235 240  
 Arg Pro Trp Ala Arg Ser Cys Ala His Gln Gly Cys Gly Ala Gly Thr  
 245 250 255  
 Arg Asn Ser

(2) INFORMATION FOR SEQ ID NO:244:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

25 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 30 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 35 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val L u Tyr Met Asp Pro Met Cys Leu Asp Ala Ph Pro Lys Leu  
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Il Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 L u Lys Ser Ser Lys Tyr Ile Ala Trp Pro L u Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys S r Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Gly Thr  
 225 230 235 240  
 5 Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu Arg Gln Ala Ser Gln  
 245 250 255  
 His

(2) INFORMATION FOR SEQ ID NO:245:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 282 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

15 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 20 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 25 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 30 Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Tyr  
 225 230 235 240  
 Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser  
 245 250 255  
 Val Arg Gly Gly Cys Gly Ala His Ser Ser Pro Pro Arg Ala Gly Arg  
 260 265 270  
 Gly Pro Arg Gly Thr Met Val Ser Arg Leu  
 275 280

35

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 262 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

5  Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
   1      5      10      15
   Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20      25      30
   Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
      35      40      45
   Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
      50      55      60
10  Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
   65      70      75
   Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
      85      90      95
   Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
      100      105      110
   Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
      115      120      125
   Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
      130      135      140
15  Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
   145      150      155
   Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
   Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
   Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
20  Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
   210      215      220
   Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser Arg Tyr
      225      230      235
   Lys His Asp Ile Gly Cys Asp Ala Gly Val Asp Lys Lys Ser Ser Ser
      245      250      255
   Val Arg Gly Gly Cys Gly
      260

```

25 (2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 264 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1      5      10      15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20      25      30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
      35      40      45
35 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
   50      55      60
   Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
   65      70      75
   Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Il S r Met Leu Glu

```

				85					90					95			
	Gly	Ala	Val	Leu	Asp	Il	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
				100					105					110			
	Lys	A	p	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
				115					120					125			
	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
				130					135					140			
5	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
10	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Gly	Cys	
	Asp	Ala	Gly	Val	Asp	Lys	Lys	Ser	Ser	Ser	Val	Arg	Gly	Gly	Cys	Gly	
	Ala	His	Ser	Ser	Pro	Pro	Arg	Ala									

(2) INFORMATION FOR SEQ ID NO:248:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

	Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
	1				5				10						15	
	Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
					20				25				30			
	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
					35				40				45			
	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
					50				55				60			
25	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
					85				90						95	
	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
					100				105					110		
	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
					115				120					125		
30	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
35	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	Gly	Ser	Pro	Gly	Ile	Pro	Gly	Ser	Thr	Arg	Ala	Ala	Ala	Ser	Gly	Ala

His Ser Ser Pro Pro Arg Ala Gly Arg Gly Pro Arg Gly Thr Met Val  
 245 250 255  
 Ser Arg Leu

(2) INFORMATION FOR SEQ ID NO:249:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

10 Ser Gly Ser Pro Pro Cys Cys Cys Ser Trp Gly Arg Phe Met Gln Gly  
 1 5 10 15  
 Gly Leu Phe Gly Gly Arg Thr Asp Gly Cys Gly Ala His Arg Asn Arg  
 20 25 30  
 Thr Ser Ala Ser Leu Glu Pro Pro Ser Ser Asp Tyr  
 35 40

(2) INFORMATION FOR SEQ ID NO:250:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Ser His Ser Gly Gly Met Asn Arg Ala Tyr Gly Asp Val Phe Arg Glu  
 1 5 10 15  
 Leu Arg Asp Arg Trp Asn Ala Thr Ser His His Thr Arg Pro Thr Pro  
 20 25 30  
 Gln Leu Pro Arg Gly Pro Asn Ser  
 35 40

25 (2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg  
 1 5 10 15  
 Ser Arg Pro Asn Gly  
 20

(2) INFORMATION FOR SEQ ID NO:252:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:



(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

5 Cys Gly Ala Gly Thr Arg Asn Ser His Gly Cys Ile Thr Arg Pro Leu  
1 5 10 15  
Arg Gln Ala Ser Ala His Gly  
20

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 15 (A) NAME/KEY: Modified Site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: "Xaa=Ser or Thr"

- (A) NAME/KEY: Modified Site  
(B) LOCATION: 3  
(D) OTHER INFORMATION: "Xaa=Arg or Lys"

- (A) NAME/KEY: Modified Site  
(B) LOCATION: 4  
(D) OTHER INFORMATION: "Xaa=Lys or Arg"

- 20 (A) NAME/KEY: Modified Site  
(B) LOCATION: 6  
(D) OTHER INFORMATION: "Xaa=Ser or Leu"

- (A) NAME/KEY: Modified Site  
(B) LOCATION: 7  
(D) OTHER INFORMATION: "Xaa=Arg, Ile, Val or Ser"

- 25 (A) NAME/KEY: Modified Site  
(B) LOCATION: 8  
(D) OTHER INFORMATION: "Xaa=Ser, Tyr, Phe or His"

- (A) NAME/KEY: Modified Site  
(B) LOCATION: 10  
(D) OTHER INFORMATION: "Xaa=Phe, His or Arg"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

30 Xaa Thr Xaa Xaa Ser Xaa Xaa Xaa Asn Xaa Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified Site  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: "Xaa=Ser, Ala or Gly"
- (A) NAME/KEY: Modified Site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: "Xaa=Val or Gln"
- 5 (A) NAME/KEY: Modified Site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: "Xaa=Pro, Gly or Ser"
- (A) NAME/KEY: Modified Site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: "Xaa=Trp or Tyr"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Asp Xaa Asp Xaa Arg Arg Xaa Xaa  
 1 5

(2) INFORMATION FOR SEQ ID NO:255:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

- 20 (A) NAME/KEY: Modified Site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: "Xaa=Ala or Phe"
- (A) NAME/KEY: Modified Site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: "Xaa=Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

25 Val Arg Ser Gly Cys Gly Xaa Xaa Ser Ser  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:256:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Asn Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg  
 1 5 10

35 (2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

5 Ser Thr Lys Arg Ser Leu Ile Tyr Asn His Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

10 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Ser Thr Gly Arg Lys Val Phe Asn Arg Arg  
1 5 10

15 (2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Thr Asn Ala Lys His Ser Ser His Asn Arg Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

30 Asp Ser Asp Val Arg Arg Pro Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

35 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Ala Ala Asp Gln Arg Arg Gly Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Asp Gly Arg Gly Gly Arg Ser Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Arg Val Arg Ser  
1

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Ser Val Arg Ser Gly Cys Gly Phe Arg Gly Ser Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Ser Val Arg Gly Gly Cys Gly Ala His Ser Ser  
1 5 10